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GenCore version 5.1.6
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- protein search, using sw model OM protein Run on:

January 10, 2005, 21:05:23; Search time 153 Seconds (without alignments) 940.199 Million cell updates/sec

US-09-813-718-10\_COPY\_71\_471

1 SNHGPDATEAEEDFVDPWTV.......VTDEIVKEFMTPRKLSFDFQ 401 score: Title: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

2002273 segs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:\*
geneseqp2001s:\*
geneseqp2002s:\*
geneseqp2003as:\*
geneseqp2003bs:\* A\_Geneseq\_23Sep04:\* geneseqp1980s:\* geneseqp1990s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:\*

## SUMMARIES

uo.	TrpRS T1	Human sup	Human sup	His6-tagg	Human sup	Human min	Human min	His6-tagg	Human min	Novel hum	Human try	Cancer/an	Marker ge	Protein e	Human ful	Human try	Full leng	Human ful	Human pro	Human hea	Human pro	Pancreas	Lung canc	Human HCM	TrpRS T2
Description	Aaq79549	Aab47617	Aae13493	Aag79548	Abu72386	Aab47616	Aae13492	Aag79547	Abu72385	Adf76576	Abu64298	Adn39916	Adj75318	Adp12573	Aab47615	Aae13491	Aag79546	Abu72384	Ade25762	Adj69429	Ade76998	Adq30575	Aab58220	Aay05372	Aag79541
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* Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	99.3	99.3	99.3	99.3	99.3	99.1	94.0
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AAB47618 5. AAE13494 AAG79544 ABJ72387 6. ABJ72387 6. ABJ72387 6. ABJ709825 7. AAG799825 7. AAG73698 7. AAG73698	ABJ2648/ 7 ADB70160 3 AAG23699
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## ALIGNMENTS

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neovascular eye disease; age-related macular degeneration; ocular complication; diabetes; rubeotic glaucoma; retinopathy; prematurity; keratitis; ischaemic retinopathy; pathological myopic; ocular histoplasmosis; pterygia; T1; punitate innerchoroidopathy; retinal degeneration; growth factor; vascularisation; vascular endothelial cell function; angiogenesis.
                                                                      tryptophanyl-tRNA synthase; TrpRS; ocular neovascularisation;
AAG79549 standard; protein; 401 AA
                                   (first entry)
                                                     TrpRS Il polypeptide.
                                   10-DEC-2002
                 AAG79549;
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22-FEB-2002; 2002WO-US005185. WO200267970-A1. Homo sapiens. 06-SEP-2002.

(SCRI ) SCRIPPS RES INST.

23-FEB-2001; 2001US-0270951P.

Friedlander Schimmel P, Wakasugi K,

Ξ

WPI; 2002-698635/75.

New polypeptides derived from human tryptophanyl-tRNA synthase, useful for inhibiting ocular neovascularization in a patient, or for treating neovascular eye diseases, e.g. rubeotic glaucoma, retinopathy, keratitis, or pterygia.

Example 1; Page 78-79; 83pp; English.

This sequence represents a novel cleavage product, T1, of recombinant human tryptophanyl-tRNA synthase (TrpRS). A related cleavage product, T2, is water soluble and comprises residues 94-471 of full length TrpRS. The water-soluble T2 polypeptide is useful for inhibiting ocular neovascularisation in a patient. T2 polypeptide is useful for treating neovascular eye diseases, e.g. age-related macular degeneration, ocular complications of diabetes, rubeotic glaucoma, retinopathy of

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Schimmel P,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tyrosyl-tRNA synthetase; TyrRS; Rossmann fold nucleotide binding domain; vascular endothelial cell function; burn; plastic surgery; abdomen; polymorphonuclear leucocyte elastase; anajogenesis; tumour metastasis; angiogenesis; graft; myocardial infarction; solid tumour; wound healing; dermal ulcer; diabetic ulcer; endothelialization;
 prematurity, keratitis, ischaemic retinopathy (e.g. sickle cell), pathological myopic, ocular histoplasmosis, pterygia, or punitate innerchoroidopathy. This polypeptide is particularly useful for treating retinal degeneration to prevent the damaging effects of trophic and growth factors, and for promoting vascularisation to retard retinal degeneration by enhancing blood flow to cells. These are also useful for regulating vascular endothelial cell function, and in particular, for
                                                                                                                                                                                                                                                 1 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH
(e.g. sickle cell),
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                                                                                                                                                                   100.0%; Score 2116; DB 5; Length 401; 100.0%; Pred. No. 1.6e-209; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dermal ulcer, diabetic ulcer, endothelialization;
tryptophanyl-tRNA synthetase; trpRS; vascular graft surgery
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                                                                                                                                                                                                       Matches 401; Conservative
                                                                                                               inhibiting angiogenesis
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The sequences given in AAB47615-18 show full length and truncated versions of trptophanyl-tENNA synthecase (TrpRS). The truncated TrpRS of the invention comprises a Rosemann fold nuclectide binding domain, and is capable of regulating vascular endothelial cell function. It is of approx. 40 kilo Dalton molecular weight and is produced by cleavage of full length TrpRS with polymorphonuclear leucocyte elastase. Truncated TrpRS is useful for regulating angiogenesis, tumor metastasis, enhancing angiogenesis to a graft, treating myccardial infarction, solid tumor, and a condition that would benefit from increased or decreased angiogenesis of a mammal, in particular humans. It is also useful in diagnosis and as a wound healing agent for treating wounds such as dermal ulcers, diabetic capables, burns and injuries and in plastic surgery when reconstruction is useful in the treatment of abdominal wounds where there is high risk of infection. Truncated TrpRS promotes endothelialization in vascular graft infection. Truncated TrpRS promotes endothelialization in vascular graft angiogenic tRNA synthetase polypeptides or polynucleotides directly to the lumen and wall of the blood vessel
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angiogenesis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 415;
                                                                       New human truncated tyrosyl-tRNA synthetase polypeptide for vascular endothelial function, in particular for regulating tumor metastasis and treating myocardial infarction.
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0; Mismatches 0;
                                                                                                                                             Disclosure, Page 129-30, 150pp; English
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Best Local Similarity 100.º
Matches 401, Conservative
                             WPI; 2001-626377/72
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                                               N-PSDB; AAH43604
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FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP 121

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The patent discloses human aminoacyl tRNA synthetases, particularly cruncated tryptophanyl-tRNA synthetases (TrpRS) comprising a Rossmann CC fold mucleotide binding domain and polynucleotides encoding them. The invention also relates to tyrosyl t-RNA synthetases (TyrRS). TrpRS sequences are useful for regulating vascular endothelial cell function, preferably angiogenesis. CC captures and diabetic ulcers, including pressure cores, venous ulcers and diabetic ulcers, burns and injuries. TrpRS sequences can also be used in plastic surgery when reconstruction is required following a burn, other trauma, or even for cosmetic purposes. Cc angiogenic TrpRS is also used in association with surgery and following the repair of cuts, for promoting endothelialisation in vascular graft conjunction with coronary bypass surgery by stimulating the growth of surgery and for repairing the damage of myocardial infarction and in cconjunction with angiography. TrpRS is also used in conjunction with angiography. TrpRS DNAs are useful in gene therapy. TrpRS antibodies are used in immunoassays to detect the presence of tumours. They are also useful for transplanted transplants presence of tumours. They are also useful for preventing further growth of solid tumours. These antibodies any also be used to treat inflammation caused by increased vascular permeability. Inhibiting the activity of TrpRS by cantisense technology is useful for preventing further growth or even regress solid tumours, and for treating rheumatoid arthritis, psortasis, diabetic retinopathy, all of which are characterised by abnormal consideration in pET20B
                                                                 TyrRS; vascular endothelial cell function; angiogenesis; wound healing; re-vascularisation; dermal ulcer; pressure sore; venous ulcer; injury; diabetic ulcer; burn; plastic surgery; cosmetic; myocardial infarction; angiography; gene therapy; tumour; inflammation; vascular permeability; rheumatoid arthritis; psoriasis; diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel truncated tryptophanyl-tRNA synthetase polypeptides capable of regulating vascular endothelial cell function, preferably angiogenesis, is useful for treating solid tumor or suppressing tumor metastasis in
                                                  synthetase;
                                                  tryptophanyl-tRNA synthetase; TrpRS; tyrosyl t-RNA
Human supermini tryptophanyl t-RNA synthetase in pET20B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 129-130; 149pp; English.
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                                                                                                                                                                                                                                                                   WO200175078-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schimmel P,
                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mammal.
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9 1 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH Gaps ; 0 100.0%; Score 2116; DB 5; Length 415; 100.0%; Pred. No. 1.7e-209; Indels . 0 0; Mismatches Conservative Similarity 401; Query Match Local Matches ð.

Sequence 415 AA;

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FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP 120 61 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH 61 ~

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptides derived from human tryptophanyl-tRNA synthase, useful for inhibiting ocular neovascularization in a patient, or for treating neovascular eye diseases, e.g. rubeotic glaucoma, retinopathy, keratitis,
                          KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL
                                                                                          VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAESFSNSFPQIFRDRTDIQCLIPCA
                                                                                                                                                               IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT
            LVIOMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN
                                                                          VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T2; tryptophanyl-tRNA synthase; TrpRS; ocular neovascularisation; neovascular egeneration; ocular emploration; diabetes; rubectic glaucoma; retinopathy; premarurity; keratitis; ischaemic retinopathy; sickle cell; pathological myopic; ocular histoplasmosis; pterygia; T1; punitate innerchoroidopathy; retinal degeneration; growth factor; vascularisation; yascular endothelial cell function; anglogenesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                His6-tagged TrpRS Il polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                               AAG79548 standard; protein; 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                             61 FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP 120
                                                                                                                                                                                                                                                                                                LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 180
pathological myopic, ocular histoplasmosis, pterygia, or punitate innerchoroidopathy. This polypeptide is particularly useful for treating retinal degeneration to prevent the damaging effects of trophic and growth factors, and for promoting vascularisation to retard retinal degeneration by enhancing blood flow to cells. These are also useful for regulating vascular endothelial cell function, and in particular, for
                                                                                                                                                                                                                                        VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
                                                                                                                                                                                                                                                                                                                                                                                                                            VVKI QKHVTFNQVKGI FGFTDSDCIGKISFPAIQAAPSFSNSFPQI FRDRTDIQCLI PCA
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                                                                                                                                                                                                                  SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH
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                                                                                                                                                         Length 415;
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                                                                                                                                                         100.0%; Score 2116; DB 5; 100.0%; Pred. No. 1.7e-209;
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                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                       Matches 401; Conservative
                                                                                               inhibiting angiogenesis
                                                                                                                                                                        Similarity
                                                                                                                            Sequence 415 AA;
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Human, tryptophanyl tRNA synthetase; TrpRS; angiogenesis; cytostatic; vulnerary; Rossmann fold nuclectide binding domain; chemokine; EMAP II; vascular endothelial cell; solid tumour; myocardial infarction; enzyme; endothelial monocyte-activating polypeptide II; tumour metastasis; wound healing; dermal ulcer; endothelialisation; vascular graft surgery;
                                                                                                                                                                                 abdominal wound; coronary bypass surgery; gene therapy
                                                                                   Human supermini Tryptophanyl tRNA synthetase/His tag.
           Ź
           ABU72386 standard; protein; 415
                                                            (first entry)
                                                                                                                                                                                                             Homo sapiens.
                                                              16-JUN-2003
                                                                                                                                                                                                                           Synthetic.
                                     ABU72386;
ABU72386
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The invention relates to an isolated polypeptide comprising a truncated tryptophanyl-tRNA synthetase (TrpRS) polypeptide comprising a Rossmann tryptophanyl-tRNA synthetase (TrpRS) polypeptide comprising a Rossmann fold model and collectivity. The isolated comprising an explain or having chemokine activity. The isolated comprising the capable of regulating vascular endothelial cell function. TyrRS has a C-terminal domain containing an EWAP II (endothelial monocyte activating polypeptide II, a proinflammatory cytokine) like domain and is similar in sequence to TrpRS. Also included are a polymucleotide concaining the TrpRS (or a polymucleotide 95% similar to it) a TrpRS epitope, concaining the TrpRS nucleic acid and expressing TrpRS, an isolated anticontaining the TrpRS nucleic acid, a recombinant vector comprising the TrpRS nucleic acid, a recombinant bost cell containing the TrpRS nucleic acid, a recombinant bost cell containing the TrpRS nucleic acid, a recombinant bost cell containing the TrpRS nucleic acid, a recombinant bost cell containing the TrpRS nucleic acid, a recombinant bost cell containing the Companies and suppressing anglogenesis, solid tumours or a condition that would benefit from decreased anglogenesis, solid tumours or a condition that composition for transdermal, transdermal, transdermal thereapeutic application of a plarmaceutical composition for transdermal, transdermal, enteral or parenteral composition for transdermal, transdermal enterated protedin. The truncated transdermal, transdermal, enteral or parenteral composition for regulating anglogenesis, for tracating myocarchial confidence, particularly for regulating anglogenesis, for tracating myocarchial confidence, and for suppressing the promotion of endothelialisation in vascular gent as entered the promotion of endothelialisation in vascular gent fer treatment of abdominal wounds where there is a high risk infection, in the composition of endothelialisation in vascular search in the cornium recompance of treatment of abdominal wound 
                                                                                                                                                            New truncated tryptophanyl-tRNA synthetase polypeptide comprising a
Rossmann fold nucleotide binding domain or having chemokine activity
useful for e.g. for regulating angiogenesis and for treating myocardial
                                                                                                                                                                                                                                                                                                             Example 1; Page 50-51; 91pp; English.
                        ×
                           Wakasugi
                                                                                 2003-340974/32.
                                                                                                         N-PSDB; ACA64107
                           Schimmel P,
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SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH Gaps ö Length 415; 100.0%; Score 2116; DB 6; 100.0%; Pred. No. 1.7e-209; 0; Mismatches Best Local Similarity 100. Matches 401, Conservative Sequence 415 AA; Query Match

conjunction with coronary bypass surgery by stimulating the growth of transplanted tissue, and in gene therapy. The present sequence is a Transplanted tissue, and in length, truncated or mutant) with a His

affinity tag

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                                               61
                                                                                   LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN
                                                                                                         LVIQMIDDEKYLWKDLILDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN
                                                                                                                                                                                       IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT
FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP
                                                                                                                                     VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
                                                                                                                                                    IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT
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360

KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL

301 302

21-MAR-2001; 2001US-00813718 21-MAR-2001; 2001US-00813718

JS2002182666-A1

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SCHIMMEL I

(SCHI/) (WAKA/)

SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH 83

263

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The sequences given in AAB47615-18 show full length and truncated versions of tryptophanyl-tRNA synthetase (TrpRS). The truncated TrpRS of the invention comprises a Rossmann fold nucleotide binding domain, and is capable of regulating vascular endothelial cell function. It is of the invention comprises a Rossmann fold nucleotide binding domain, and is processed to the invention capable of regulating vascular endothelial cell function. It is of thill length TrpRS with polymorphonuclear leucocyte elastase. Truncated CT firsts is useful for regulating angiogenesis, tunor metastasis, enhancing angiogenesis to a graft, treating myccardial infarction, solid tunor, and can confition that would benefit from increased or decreased angiogenesis of a condition that would benefit from increased or decreased angiogenesis of in a mammal, in particular humans. It is also useful in diagnosis and as a wound healing agent for treating wounds such as dermal ulcers, diabetic culcers, burns and injuries and in plastic surgery when reconstruction is crequired following a burn or for cosmetic purposes. It is particularly useful in the treatment of abdominal wounds where there is high risk of infection. Truncated TrpRS promotes endothelialization in vascular graft surgery and is used in conjunction with angiography to administer the angiogenic tRNA synthetase polypeptides or polynucleotides directly to the lumen and wall of the blood vessel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human truncated tyrosyl-tRNA synthetase polypeptide for regulating vascular endothelial function, in particular for regulating angiogenesis, tumor metastasis and treating myocardial infarction.
                                                                                                                                                                                                                                                                                                                   Tyrosyl-tRNA synthetase; TyrRS; Rossmann fold nucleotide binding domain; vascular endothelial cell function; burn; plastic surgery; abdomen; bolymorphonuclear leucocyte elastase; angiogenesis; tumour metastasis; angiogenesis; graft; myocardial infarction; solid tumour; wound healing; dermal ulcer; diabetic ulcer; endothelialization; tryptophanyl-tRNA synthetase; trpRS; vascular graft surgery.
  401
                 Disclosure; Page 123-24; 150pp; English.
                                                                                                                                                   Ź
                                                                                                                                                AAB47616 standard; protein; 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAR-2001; 2001WO-US008966
                                                                                                                                                                                                                                       entry)
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                                                                                                                                                                                                                                                                             Human mini TrpRS
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                                                                                                                                                                                                                                   07-JAN-2002
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FIRRGIFFSHRDMNQVLDAXENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP 143
                                                                            LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 180
                                                                                             LVIQMTDDEKYLWKDLTLDQAYGDAVGNAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 203
                                                                                                                                             VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA 240
                                                                                                                                                                                                               241 IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300
                                                                                                                                                                                                                                    KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 360
                                                                                                                                                                                                                                                                                                     KVNKHAFSGGRDTIEEHRQFGGCNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, tryptophanyl-tRNA synthetase; TrpRS; tyrosyl t-RNA synthetase; TyrRS; vascular endothelial cell function; angiogenesis; wound healing; re-vascularisation; dermal ulcer; pressure sore; venous ulcer; injury; diabetic ulcer; burn; plastic surgery; cosmetic; myocardial infarction; angiography; gene therapy; tumour; inflammation; vascular permeability; rheumatoid arthritis; psoriasis; diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The patent discloses human aminoacyl tRNA synthetases, particularly truncated tryptophanyl-tRNA synthetases (TrpRS) comprising a Rossmann fold nucleotide binding domain and polynucleotides encoding them. The invention also relates to trycosyl t-RNA synthetases (TyrRS). TrpRS sequences are useful for regulating vascular endothelial cell function,
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                                                                                                                                                                 VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
          FLRRGI FFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLI PFI FTKWLQDVFNVP
                                                                                                                                                                                                                                                                                                                                                     401
                                                                                                                                                                                                                                                                                                                                                                       KKALIEVLQPLIAEHQARRKEVIDEIVKEFMTPRKLSFDFQ 424
                                                                                                                                                                                                                                                                                                                                                     KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human mini tryptophanyl t-RNA synthetase in pET20B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE13492 standard; protein; 437 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-FEB-2002 (first entry)
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N-PSDB; AAD22483.
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100.0%; Score 2116; DB 4; Length 437; 100.0%; Pred. No. 1.8e-209;

al Similarity 100. 401; Conservative

Query Match Local Matches punitate innerchoroidopathy, retinal degeneration; growth factor; vascularisation; vascular endothelial cell function; angiogenesis

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equences can also be used in plastic surgery when reconstruction is required following a burn, other trauma, or even for cosmetic purposes.

Angiogenic TrpRS is also used in association with surgery and following the repair of cuts, for promoting endothelialisation in vascular graft surgery and for repairing the damage of myocardial infarction and in conjunction with coronary bypass surgery by stimulating the growth of transplanted tissue. TrpRS is also used in conjunction with angiography.

TrpRS DNAs are useful in gene therapy. TrpRS antibodies are used in immunoassays to detect the presence of tumours. They are also useful for blocking endogenous angiogenic activity and retard the growth of solid tumours. These antibodies may also be used to treat inflammation caused by increased vascular permeability. Inhibiting the activity of TrpRS by antisense technology is useful for preventing further growth or even regress solid tumours, and for treating rhemmatoid arthritis, psoriasis, and adabetic retinopathy, all of which are characterised by abnormal angiogenesis. The present sequence is human truncated tryptophanyl t-RNA surfaces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
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preferably anglogenesis. Anglogenic TrpRS sequences are useful as wound healing agents for re-vascularising damaged tissues. They are useful for treating full-thickness wounds (e.g. dermal ulcers, including pressure sores, venous ulcers and diabetic ulcers), burns and injuries. TrpRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMTVGHLIPFIFTKWLQDVFNVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 437;
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New polypeptides derived from human tryptophanyl-tRNA synthase, useful for inhibiting ocular neovascularization in a patient, or for treating neovascular eye diseases, e.g. rubeotic glaucoma, retinopathy, keratitis,

Schimmel P, Wakasugi K, Friedlander M;

WPI; 2002-698635/75. N-PSDB; ABA00329.

22-FEB-2002; 2002WO-US005185. 23-FEB-2001; 2001US-0270951P. (SCRI ) SCRIPPS RES INST

WO200267970-A1 Homo sapiens.

06-SEP-2002

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This sequence represents a His6-tagged cleavage product, mini-TrpRS, of recombinant human tryptophanyl-tRNA synthase (TrpRS). A related cleavage recombinant human tryptophanyl-tRNA synthase (TrpRS). A related cleavage product, T2, is water soluble T2 polypeptide is useful for inhibiting collar neovascular expension in a patient. The T2 polypeptide is useful for inhibiting collar neovascular eye diseases, e.g. age-related macular degeneration, collar complications of diabetes, rubeotic glaucoma, retinopathy of prematurity, keratitis, ischemic retinopathy (e.g. sickle cell), collar histoplasmosis, pterygia, or punitate innerchoroidopathy. This polypeptide is particularly useful for treating crimal degeneration to prevent the damaging effects of trophic and corp promoting vascularisation to retard retinal degeneration by enhancing blood flow to cells. These are also useful for regulating vascular endothelial cell function, and in particular, for inhibiting anglogenesis
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100.0%; Score 2116; DB 5;
Best Local Similarity 100.0%; Pred. No. 1.8e-209;
Matches 401; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                   Example 3; Fig 1; 83pp; English.
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                                                                                                                                                                                                                                                                                                                            or pterygia.
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T2; tryptophanyl-tRNA synthase; TrpRS; ocular neovascularisation; neovascular eye disease; age-related macular degeneration; ocular complication; diabetes; rubbotic glaucoma; retinopathy; prematurity; keratitis; ischaemic retinopathy; sickle cell; pathological myopic; ocular histoplasmosis; pterygia;

His6-tagged mini-TrpRS polypeptide.

(first entry)

10-DEC-2002

AAG79547;

AAG79547 standard; protein; 437

RESULT 8 AAG79547

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The invention relates to an isolated polypeptide comprising a truncated tryptophanyl-tRNA synthetase (TrpRS) polypeptide comprising a Rossmann Cold mucleotide binding domain or having chemokine activity. The isolated polypeptide is capable of regulating vascular endochelial cell function. TyrRS has a C-terminal domain containing an EWAP II (endothelial menocyterating polypeptide II, a proinflammatory vtokine)-like domain and is similar in sequence to TrpRS. Also included are a polymucleotide containing the TrpRS (or a polymucleotide 95% similar to it) a TrpRS spitope, comprising an isolated TrpRS pulymucleotide, a recombinant vector comprising the TrpRS nucleic acid and expressing TrpRS, an isolated anticontaining the TrpRS nucleic acid and expressing TrpRS, an isolated anticontaining the TrpRS nucleic acid and expressing TrpRS, an isolated anticontaining the TrpRS nucleic acid and expressing trpRS, an isolated anticontaining the TrpRS nucleic acid and expressing TrpRS, and suppressing anglogenesis, solid tumours or a condition that would benefit from decreased anglogenesis, solid tumours or a condition that would benefit from decreased anglogenesis, solid tumours acondition that composition for transdermal, transmucosal, enteral or parenteral administration. The truncated tRNA synthetase polypeptide is useful for regulating vascular endothelial cell function, particularly for regulating anglogenesis, for treating myocardial infarction and solid tumour, and for suppressing tumour metasteasis.

Anglogenic tRNA synthetase polypeptides are useful as wound healing agents or for treating full thickness wounds such as dermal ulcers, in the promotion of endothelialisation in vascular graft surgery, in the
                                                                                                                                                                                                                                                                                                          Human; tryptophanyl tRNA synthetase; TrpRS; angiogenesis; cytostatic; vulnerary; Rossmann fold nucleotide binding domain; chemokine; EMAP II; vascular endothelial cell; solid tumour; myocardial infarction; enzyme; endothelial monccyte-activating polypeptide II; tumour metastasis; wound healing; dermal ulcer; endothelialisation; vascular graft surgery; abdominal wound; coronary bypass surgery; gene therapy.
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                                         424
Human mini Tryptophanyl tRNA synthetase/His tag.
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                                                                                                                                            ABU72385 standard; protein; 437
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treatment of abdominal wounds where there is a high risk infection, in conjunction with coronary bygass surgery by stimulating the growth of th transplanted tissue, and in gene therapy. The present sequence is a Trp tRNA synthetase protein (full length, truncated or mutant) with a His
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                                                                                                                     Length 437;
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Pred. No. 1.8e-209;
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Human tryptophanyl-tRNA synthetase protein.

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This invention relates to novel nucleic acids encoding human PRO secreted and transmembrane proteins. Extracellular proteins play important roles in the formation, differentiation and maintenance of multicellular corganisms. The fate of many individual cells (for example proliferation, migration or differentiation) is typically governed by information.

Crecived from other cells and the immediate environment. The information crecived from other cells and the immediate environment. The information of solution or differentiation of sectors, crecived for example mitogenic factors, crecived from tangentics, crecived and interpreted by diverse cell receptors or membrane bound proteins. These membrane bound proteins and receptors may be of use as pharmaceutical and diagnostic agents, such as in the blocking of receptor-ligand interactions. The current invention provides the amino acid sequences of novel human membrane bound receptors and proteins of the invention may have cytostatic activities through the stimulation of chondrocytes. The nucleic acids of the invention may be useful for the manufacture of a medicament for diagnosing or treating at tumour in a mammal. In addition, they may be useful for measuring or detecting the expression of a tumour associated gene. The present
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                         New PRO polypeptides, useful for diagnosing and treating an immune related disorder, e.g. systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or diabetes mellitus.
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Matches 401; Conserv
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N-PSDB; ADF76575
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KVNKHAFSGGRDTIEBHROFGGNCDVDVSFMYLTFFEEDDDKLEQIRKDYTSGAMLTGEL 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 LVIQMIDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to an adeno-associated viral (AAV) vector comprising a polymucleotide that comprises a nucleic acid segment that encodes a choroidal or ocular neovascularisation inhibitory polypeptide operably linked to a promoter that expresses the segment to produce the polypeptide in a selected mammalian host cell. Such a vector is useful for providing a choroidal or ocular neovascularisation inhibitory polypeptide to a mammal, for use in the therapy of coular neovascularisation, choroidal neovascularisation, retinal neovascularisation, age-related macular degeneration, visual impairment, coular dysfunction, loss of vision, retinopathy, or blindness in a human. The present sequence is a protein shown in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                              Novel adeno-associated viral vector comprising polynucleotide encoding pigment epithelium-derived factor, useful for treating choroidal neovascularization, blindness, loss of vision.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 İVIÇMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                   Vector; rAAV; recombinant adeno-associated viral vector; anti-anglogenesis; PEDF; anglogenesis; eye disorder; blindness; retinal degeneration; macular degeneration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 2116; DB 7;
Best Local Similarity 100.0%; Pred. No. 2.1e-209;
Matches 401; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                    Hauswirth WW, Campochiaro PA, Berns
                                                                                                                                                                                                                                                                                    (UYFL ) UNIV FLORIDA RES FOUND INC. (UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 14; Page 46; Opp; English
                                                                                                                                                                                                                       20-MAR-2003; 2003WO-US008667.
                                                                                                                                                                                                                                                       20-MAR-2002; 2002US-0366114P.
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-779243/73.
N-PSDB; AAL56267.
                                                                                             ophthalmological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 471 AA;
                                                                                                                                                             WO2003080648-A2
                                                                                                                              Homo sapiens
                                                                                                                                                                                          02-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention
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ABU64298 standard; protein; 471

11-MAR-2004 (first entry)

ABU64298;

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polypeptide of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, and nucleic acids in the nucleic acids, polypeptides, antibodies and methods are useful for diagnosing, prognosing and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atterosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularistaion syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 251 VVXIQXHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KVNKHAPSGGRDTIBEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bronchial asthma; chronic obstructive pulmonary disease;
respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLRRGIFFSHRDMQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT
                                                                                                                                                                                                                                                                                                                                                                                                     1 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH
  nucleic acid of the invention; antibodies which specifically bind a
                                                                                                                                                                                                                                                                                                      Length 471;
                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marker gene related amino acid sequence SEQ ID NO:570
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                                                                                                                                                                                                                                                                                                    100.0%; Score 2116; DB 7;
100.0%; Pred. No. 2.1e-209;
ive 0; Mismatches 0;
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20-MAR-2003; 2003JP-00077212.
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Matches 401; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene therapy; marker.
                                                                                                                                                                                                                                                          Sequence 471 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP1394274-A2
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                                                                                                                                                                                                                                                                                                         Query Match
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371 KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 430
                                                                                                                                                                                                                                                                                                                                                                                                Human; differential expression; cancer; angiogenic disorder; fibrotic disorder; psoritasis; isofatemia; heart disease; atherosclerosis; inflammatory disease; autoimmune disease; retinal neovascularistaion syndrome; scarring; uterine fibroid; detection; diagnosis; prognosis; drug screening; drug targeting; wound healing; contraception; cytostatic; cardiant; immunomodulatory; vulnerary; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to nucleic acids and proteins (ADN18683-ADN40064) whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a
                                                                                                                                                                                                                                                                                                                                                       Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:C286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hevezi PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glynne R,
3, Zlotnik
                                                                    KKALIBVLQPLIAEHQARKEVTDEIVKEFMTPRKLSFDFQ
                                              KKALIEVLOPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ
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Wilson KE,
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                                                                                                                                                                                                            ADN39916 standard; protein; 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ginsburg WM,
R, Watson SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-NOV-2001; 2001US-0350666P.
21-NOV-2001; 2001US-0332464P.
29-NOV-2001; 2001US-0334393P.
03-DEC-2001; 2001US-0334394P.
14-DEC-2001; 2001US-0340376P.
10-JAN-2002; 2002US-0347349P.
10-JAN-2002; 2002US-0347349P.
13-PEB-2002; 2002US-0355250P.
13-PEB-2002; 2002US-0355250P.
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29-MAR-2002; 2002US-0358809P.
04-APR-2002; 2002US-0370110P.
05-JIN-2002; 2002US-03701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EOSB-) EOS BIOTECHNOLOGY INC
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09-SEP-2002; 2002US-0409450P.
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                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-468649/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADN39699
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22-JUL-2002;
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Mack DH,
                                                                                                                                                                                                                                                          ADN39916;
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disease by

Izuhara

Nagai H,

The present invention describes a method of testing for bronchial asthma or chronic obstructive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a bubject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy subject, and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; Also described: (l) a reagent (l) for cetting for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent (c) or treat bronchial asthma or chronic obstructive pulmonary disease; (3) an animal model for bronchial asthma or chronic obstructive pulmonary disease; (5) a marker gene or an antisense nucleic acid corresponding to a portion of the marker gene or an antisense nucleic acid corresponding to a portion of costine encoded by a marker gene; a ribozyme, a polynucleotide that suppresses the probe has been immobilised to assay a marker gene; on which a probe has been immobilised to assay a marker gene, on which a probe has been immobilised to assay a marker gene, on the present corresponding for or screening for a therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease, on which a probe has been immobilised to assay a marker gene, and antiasthmatic activities, and can be used in gene therapeutic agent for bronchial asthma or chronic obstructive pulmonary disease. The present corresponding for or screening for a therapeutic agent invention. comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a for bronchial asthma or chronic obstructive pulmonary Example 11; SEQ ID NO 570; 241pp; English Kubo H, **Үатауа** М, Sugita Y, WPI; 2004-193155/19 healthy subject. ž **Testing** Ohtani 

Sequence 471 AA;

250 71 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH 130 240 IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300 KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 360 09 LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGORPHH FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP LVIOMTDDEKYLWKDLTLDQAYGDAVENAKDIJACGFDINKTFIFSDLDYMGMSSGFYKN **VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA** Gaps ; 0 Length 471; 0; Indels 401 KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 100.0%; Score 2116; DB 8; 100.0%; Pred. No. 2.1e-209; iive 0; Mismatches 0; al Similarity 100. 401; Conservative Query Match Best Local S Matches 401 361 61 131 121 191 181 241 301 g qq g ઠે ď δ 셤 ઠે ò ð

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Similarity

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Query Match

401;

Sequence 471 AA;

LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 180

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121

FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP

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음. 성

Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, as sonotransplant rejection or mechanical organ replacement rejection, in an individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring an individual trovolve the immune system, e.g. rheumatoid arthritis, lupus, inflammatory bowel diseases multiple sclerosis, HIV/AIDS or viral, bacterial or fungal infection. The present sequence represents a protein that is encoded by the mRNA of the invention. transplant rejection; immune system; rheumatoid arthritis; lupus; inflammatory bowel disease; multiple sclerosis; HIV; AIDS. Morris M; Ly N, Prentice J, 471 431 KKALIEVLQPLIABHQARRKEVTDBIVKBFMTPRKLSFDFQ Protein encoded by mRNA of the invention #183. claim 65; SEQ ID NO 2582; 1762pp; English. Woodward R, (EXPR-) EXPRESSION DIAGNOSTICS INC. Z ADP12573 standard; protein; 471 24-APR-2003; 2003WO-US012946. 24-APR-2002; 2002US-00131831. 20-DEC-2002; 2002US-00325899. (first entry) Wohlgemuth J, Fry K, WPI; 2004-400724/37. WO2004042346-A2. Homo sapiens. Rosenberg S; 12-AUG-2004 21-MAY-2004 geneg. ADP12573; the RESULT 14 ADP12573 

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The sequences given in AAB47615-18 show full length and truncated versions of trptophanyl-tRNA synthetase (TrpRS). The truncated TrpRS of the invention comprises a Rossmann fold nucleotide binding domain, and is capable of regulating vascular endothelial cell function. It is opprox. 40 kilo Dalton molecular weight and is produced by cleavage of full length TrpRS with polymorphonuclear leucocyte elastase. Truncated full length TrpRS with polymorphonuclear leucocyte elastasis, enhancing angiogenesis to a graft, treating angiogenesis, tumor metastasis, enhancing angiogenesis to graft, treating myocardial infarction, solid tumor, and a condition that would benefit from increased or decreased angiogenesis in a mammal, in particular humans. It is also useful in diagnosis and as a wound healing agent for treating wounds such as dermal ulcers, diabetic ulcers, burns and injuries and in plastic surgery when reconstruction is required following a burn or for cosmetic purposes. It is particularly useful in the treatment of abdominal wounds where there is high risk of infection. Truncated TrpRS promotes endothelialization in vascular graft surgery and is used in conjunction with angiography to administer the
                                                                                                                         370
                                                                                                                                                                                         KVNKHAFSGGRDTIEEHRQFGGNCDVDSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 430
                                                                                 IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300
                                                                                                                                                           KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human truncated tyrosyl-tRNA synthetase polypeptide for regulating vascular endothelial function, in particular for regulating angiogenesis, tumor metastasis and treating myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tyrosyl-tRNA synthetase; TyrRS; Rossmann fold nucleotide binding domain; vascular endothelial cell function; burn; plastic surgery; abdomen; polymorphonuclear leucocyte elastase; angiogenesis; tumour metastasis; angiogenesis; graft; myocardial infarction; solid tumour; wound healing; dermal ulcer; diabetic ulcer; endothelialization; tryptophanyl-tRNA synthetase; trpRS; vascular graft surgery.
                                                                                                      IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT
                       VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDKTDIQCLIPCA
  VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
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                                                                                                                                                                                                                                                                                                                                                                                         AAB47615 standard; protein; 484 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human full-length TrpRS.
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                                                                                                                                                                                                                            LVIOMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN
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                                                                  Length 484;
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                                                               ; Score 2116; DB 4;
; Pred. No. 2.1e-209;
0; Mismatches 0;
                                                                  100.0%;
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                                                                              Similarity
                                        Sequence 484 AA;
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protein search, using sw model OM protein January 10, 2005, 21:14:03; Search time 40 Seconds (without alignments) 964.573 Million cell updates/sec Run on:

US-09-813-718-10\_COPY\_71\_471

Perfect score:

2116 1 SNHGPDATEAEEDFVDPWTV......VTDEIVKEFWTPRKLSFDFQ 401 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 DB seq DB seq Minimum I Maximum I Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	tryptophan-tRNA li	tryptophan-tRNA li	٦	tryptophan-tRNA li	hypothetical prote	tryptophan-tRNA li	tryptophanyl-tRNA	tryptophanyl-tRNA	tryptophan-tRNA li	tryptophanyl-tRNA	tryptophan-tRNA li	tryptophan-tRNA li	tryptophan-tRNA li	tryptophanyl-tRNA	probable tryptopha	tryptophanyl-tRNA	tyrosyl-tRNA synth	probable tyrosyl-t	tryptophanyl-tRNA	tryptophan-tRNA li	z	tyrosine-tRNA liga	tyrosine-tRNA liga	tryptophan-tRNA li	tryptophanyl-tRNA	tryptophan-tRNA li	protein F3M18.22 [	tryptophan-tRNA li	probable tyrosyl-t
SUMMARIES	OI	A41706	YWBO	YWRBPR	S50053	S58157	S51901	C90190	C75020	G71206	G84373	F64476	E69131	T43806	E69461	D72477	F84371	H69346	E72512	D95260	G98125	B86633	A45999	S75410	H70385	E75438	B71496	A86410	E70100	C84750
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tryptophan-tRNA li tvrosvl-tRNA synth	tryptophanyl-tRNA	tryptophanyl	tryptopnan-twnA 11 tyrosyl-tRNA synth	probable tyrosine-	tryptophan-tRNA li	tyrosine-tRNA liga	tryptophan-tRNA li	tyrosine-tRNA liga	tryptophan-tRNA 11	tryptophanyl-tRNA	tryptophan-tRNA li	tryptophan-tRNA li
F71300 B75072	C81654 T44994	H86590	C72034 C84374	T03741	E64676	F71093	AI1066	H69102	C72370	E82052	S73024	YWBSF
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337	346	344	327	408	339	375	337	319	328	365	343	328
2.5	7.5	2.0	7.7	7.1	6.9	6.9	6.9	6.5	6.4	6.4	6.3	6.2
159.5	158	152	149.5	149.5	146	146	145	138	135.5	135	132.5	132
30	32	4.0	3 P	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

	[similarit
	ophan-tRNA ligase (EC 6.1.1.2) (similarit
	ligase (
9	ophan-tRNA

N;Alternate names: interferon-inducible protein IFP53; peptide-chain release factor homo cy] - human

C;Species: Homo sapiens (man) C;Date: 19-May-2000 #sequence revision 19-May-2000 #text change 09-Jul-2004 C;Accession: A41633; A41706; \$19246; JN0676; JH0533; S26287

R.Fleckner, J.; Rasmussen, H.H.; Justesen, J. Proc. Natl. Acad. Sci. U.S.A. 88, 11520-11524, 1991 A.Title: Human interferon gamma potently induces the synthesis of a 55-kDa protein (gamm A.Reference number: A41633; WUID:92107982; PMID:1763065

A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cossereferences: UNIPROT: P23381; GB: X59892; NID: g30820; PIDN: CAA42545.1; PID: g30821
A;Cross-references: UNIPROT: P23381; GB: X59892; NID: g30820; PIDN: CAA42545.1; PID: g30821
B;Rubin, B.Y.; Anderson, S.L.; Xing, L.; Powell, R.J.; Tate, W.P.
A;Title: Interferon induces tryptophanyl-tRNA synthetase expression in human fibroblasts
A;Reference number: A41706; MUID: 92105071; PMID: 1761529

A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-471 <RUB>

A;Cross-references: GB:M77804; NID:g184656; PIDN:AAA67324.1; PID:g184657
R;Buwitt, U.; Flohr, T.; Boettger, E.C.
BRBO J. 11, 489-496; 193
A;Title: Molecular cloning and characterization of an interferon induced human cDNA with A;Reference number: S19246; MUID:92164636; PMID:1537332

, Accession: S19246

A, Status: preliminary A, Molecule type: mRNA

A; Residues: 1.423, R., 425-471 <BUW>
A; Cross-references: EMBL:X62570; NID:g32708; PIDN:CAA44450.1; PID:g32709
A;Note: 213-Ser and 214-Tyr were also found
F;rolova, L.Y.; Grigorieva, A.Y.; Sudomoina, M.A.; Kisselev, L.L.
Gene 128, 237-245, 1993
A;Title: The human gene encoding tryptophanyl-tRNA synthetase: Interferon-response elemental complex: JN0676; MUID:9329292; PMID:7685728

A; Accession: JN0676

A; Molecule type: DNA A; Residues: 1-141;182-471 <FRO1>

A;Cross-references: GB:X67918; GB:S62837; NID:g37968; GB:X67919; NID:g37969; GB:X67920; A; NID:g37974; GB:X67925; GB:X679

R, Frolova, L.Y.; Sudomoina, M.A.; Grigorieva, A.Y.; Zinovieva, O.L.; Kisselev, L.L.

Gene 109, 291-296, 1991 A;Title: Cloning and nucleotide sequence of the structural gene encoding for human trypt: A;Reference number: JH0533; MUID:92112058; PMID:1765274

A; Accession: JH0533 A; Molecule type: mRNA

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C.Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis
F;24-69/Domain: amino acid-tRNA ligase repeat homology <ATL>
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Best Local Similarity 95.8
Matches 384; Conservative
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Liyptophan-tRNA ligase (EC 6.1.1.2) [validated] - bovine
Liyptophan-tRNA ligase (EC 6.1.1.2) [validated] - bovine
N;Alternate names: tryptophanyl-tRNA synthetase
C;Species: Bos primigenius taurus (cattle)
C;Accession: A40279; UN0354; Sl0460; S14540
R;Garret, M.; Pajor, B.; Trezeguet, V.; Labouesse, J.; Merle, M.; Gandar, J.C.; Benedett
Biochemistry 30, 7809-7817, 1991
A;Title: A mammalian tryptophanyl-tRNA synthetase shows little homology to prokaryotic 8
A;Accession: A40279; MUID:91329348; PMID:1907847
A;Accession: A40279
A;Molecule type: mRNA
A;Reference number: A40279; MUID:91329348; PMID:1907847
A;Cross-references: UNIPROT:P17248; GB:M74074; EMBL:X53918; NID:g163798; PIDN:AAA30799.1
A;Cross-references: UNIPROT:P17248; GB:M74074; EMBL:X53918; NID:g163798; PIDN:AAA30799.1
A;Experimental source: pancreas
A;Note: the authors translated the codon CTG for residue 347 as Ala and CAG for residue
A;Note: the authors translated the codon CTG for residue 347 as Ala and CAG for residue
A;Note: the authors translated the codon CTG for residue 347 as Ala and CAG for residue
A;Note: the authors translated the codon CTG for residue 347 as Ala and CAG for residue
A;Note: the authors did sequence of several peptides of tryptophanyl-tRNA synthetase from ca
A;Note: the paper in this sequence of several peptides of tryptophanyl-tRNA synthetase from Ca
A;Accession: JN0354; MUID:90211408; PMID:2631684
A;Accession: JN0354; MUID:90211408; PMID:2631684
A;Molecule type: protein
A;Notec: this paper is in Russian
C;Superfamily: mammalian tryptophan-tRNA ligase repeat homology
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
                            A,Residues: 1-212,'GD',215-471 <FRO2>
A;Cross-references: GB:M61715; NID:g340367; PIDN:AAA61298.1; PID:g340368
A;Cross-references: GB:M61715; NID:g340367; PIDN:AAA61298.1; PID:g340368
C;Ganetics:
A;Gene: GDB:WARS; IFP53
A;Gross-references: GDB:119632; OMIM:191050
A;Gross-references: GDB:119632; OMIM:191050
A;Map position: 14623-14431
A;Introns: 33/3; 105/1; 141/2; 181/2; 242/2; 276/1; 313/3; 371/3; 418/3
A;Introns: 33/3; 105/1; 141/2; 181/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/2; 141/
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match

99.3%; Score 2101; DB 1;
Best Local Similarity 99.5%; Pred. No. 6.2e-162;
Matches 399; Conservative 0; Mismatches 2;
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YWKBERN

I TYPOTOPHAN-TRNA ligase (EC 6.1.1.2) [validated] - rabbit

I TYPOTOPHAN-TRNA ligase (EC 6.1.1.2) [validated] - rabbit

N;Alternate names: tryptophanyl-tRNA synthetase
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Accession: A33904; 837336
C;Accession: A33904; 837336
R;Lee, C.C.; Craigen, W.J.; Marny, D.M.; Harlow, E.; Caskey, C.T.
R;Lee, C.C.; Craigen, W.J.; Marny, D.M.; Harlow, E.; Caskey, C.T.
R;Lee, C.C.; Craigen, W.J.; Marny, D.M.; Harlow, E.; Caskey, C.T.
A;Reference number: A35904; MUID:90239043; PMID:2185472
A;Reference number: GE:M33460
A;Residues: 1-475 <LEE>
A;Cross-references: GE:M33460
A;Residues: 1-475 <LEE>
A;Cross-references: GE:M33460
A;Residues: 1-4013-4019, 1993
A;Title: Mammalian polypeptide chain release factor and tryptophanyl-tRNA synthetase are A;Accession: S37396
A;Accession: S37396
A;Accession: S37396
A;Accession: S37396
A;Accession: S37396
A;Accession: S37396
A;Accession: S37396
A;Accession: CS7396
A;Accessi
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1717/Region: ATP-binding motif (HXGH)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVKI QKHVTFNQVKGI FGFTDSDCIGKI SFPA I QAAPSFSNSFPQI FRDRTDI QCLI PCA
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2028.5; DB 1;
NO. 4.6e-156;
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90.8%; Pred. No. 1.9e-149;
tive 21; Mismatches 15;
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                     Score 2028.5;
Pred. No. 4.6e
8; Mismatches
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61

241

181

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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: 1995 cGEN>
A;Cross-references: UNIPROT:Q09692; EMBL:Z50142; NID:g1052783; PIDN:CAA90500.1; PID:g1055
R;Gentles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
A;Reference number: Z21799
A;Accession: T38561
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A;Experimental source: strain 972h-; cosmid c2F7
                                                                                                                                                                                                                          196 VIQMSDDEKYLWKDLTLEQAYSYTVENAKDIIACGFDINKTFIFSDLEYMGQSPGFYRNV 255
                                                                                                                                                                                                                                                                                                                                                                                                                                              256 VKIQKHVTFNQVKGIFGFTDSDCIGKSSFPAVQAAPSFSNSFPKIFRDRTDIQCLIPCAI 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 DQDPYFRMTRDVAPRIGHPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKSK 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELK 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein SPAC2F7.13c - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S58157; T38561
R;Gentles, S.; Churcher, C.M.
R;Gentles, S.; Churcher, C.M.
A;Reference number: S58145
A;Accession: S58157
                                                                                                                    4 EEQIVIPWDVKGSIVDGEEKGIDYERLIVQFGTRKITPEQLERFEKLTGKKPHLLLRRGA
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                                                                                                                                                                                                                                                                                                      VIOMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKNV
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  90.8%; Pred. No. 9.6e-149; ive 21; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-395 <GE2>
                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Gene: SPDB:SPAC2F7.13c
     Local Similarity
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$55003
tryptophan-tRNA ligase (BC 6.1.1.2) alpha-2 chain - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: O'-May-1995 #sequence_revision lo-Nov-1995 #text_change 09-Jul-2004
C;Accession: $50053; 19991; $31461; $31462
J. Mol. Biol. 224; $99-Gio, 1999
A;Title: An alternative splicing modifies the C-terminal end of tryptophanyl-tRNA synthe
A;Reference number: $50052; MUID:95018226; PMID:7932716
A;Accession: $50053
A;Accession: $50053
A;Accession: $50052
A;Accession: $70052
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240
                                                                                                                                                                                                                                                                                                                                                            IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQDAQTKMSASDPNSSIFLTDTAKQIKT 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYSSGAMLTGEL 434
                                                                                                                                          135 FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPPIFTKWLQDVFDVP 194
                                                                                                                                                                                                                    LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 180
                                                                                                                                                                                                                                                IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 360
                                                                                                                                                                                                                                                                                                                             VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-481 - RES>
A;Cross-references: EMBL:X69657; NID:g55437; PIDN:CAA49348.1; PID:g55438
C;Genetics: 4LSF>
A;Gene: WRS
A;Introns: 475/2
A;Note: the list of introns may be incomplete; clone W13
C;Genetics: <SSF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 401
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126 123

99 63

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Lryptophanyl-tRNA synthetase (trpS) [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: 24-May-2001 #text_change 15-Jun-2001 C;Ancession: C91990 C;Accession: C91990 C;Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-P Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
AyDescription: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE006641; NID:g13813608; PIDN:AAK40778.1; GSPDB:GN00155 C;Genetics: A;Gene: trpS C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 YFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKH 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDEKYLWK-DLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKNVVKIQ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDEKYMRNPEFILDQTRSWAYDNILDIIAVGFNPDKTFIFQDTEXI---RNMYPITVKIA 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
                                                                                                                         IDODPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300
                                                                                                                                                                                               AFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDD-KLEQIRKDYTSGAMLTGELKKAL 364
79 LRKGLFFSERDFTKILDLYEQGKPFFLYTGRGPSSDSMHLGHMIPFVFTKWLQEVFDVPL 138
                                   122 VIQMTDDEKYLWK-DLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 180
                                                     KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 VVKIQKHVTENQVKGIFGFIDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TEAEEDFVDPWTVQTSSAKG-IDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMT
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ilarity 48.6%; Pred. No. 1.5e-65;
Conservative 68; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                      361 KKALIEVLOPLIAEHQARRKEVTDEIVKEFMTPRKL 396
                                                                                                                                                                                                                                                                                                                                        IEVLOPLIAEHQARRKEVTDEIVKEFMTPRKLS 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: A99139
A;Accession: C90190
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Best Local Similarity
Matches 191; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-386 <KUR>
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SS1901
Livyptophan-tRNA ligase (EC 6.1.1.2) [similarity] - yeast (Saccharomyces cerevisiae)
Livyptophan-tRNA ligase (EC 6.1.1.2) [similarity] - yeast (Saccharomyces cerevisiae)
Livyptophanyl-tRNA synthetase
C, Species: Saccharomyces cerevisiae
C, Species: Saccharomyces cerevision 03-Aug-1995 #text_change 09-Jul-2004
C, Accession: S51901; S59177; S66793
R, Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
submitted to the EMBL Data Library, January 1995
A, Description: Sequence analysis of a 44kb DNA fragment of yeast chromosome XV including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: UNIPROT:Q12109, EMBL:Z48149; NID:g663234, PIDN:CAA88164.1; PID:g6632 R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F. F. Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F. Vastt II, 1069-1075, 1995
A;Title: Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including the a delta element.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acid-tRNA ligase repeat homology
                                                                                                                                                                                                 LRRGIFFSHRDMAQVLDAYENKKPPYLYTGRQPSSEAMHVGHLIPFIFTKWLQDVFNVPL 121
                                                         245
                                                                                            241
                                                                                                                             YFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKH 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a delta element.
A;Reference number: S59156; MUID:96076631; PMID:7502582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gross-references: SGD:SNS1; MRS1; MIPS:YOL097c
A; Cross-references: SGD:SN005457
A; Map position: 15L
C; Superfamily: mammalian tryptophan-tRNA ligase; amino C; Keywords: ligase
F;117-120/Region: ATP-binding motif (HXGH)
                                                                                                                                                                                                                                                                                            EVLOPLIAEHQARRKEVTDEIVKEFMT-PRKLSF 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: S51848
A;Accession: S51901
A;Molecule type: DNA
A;Residues: 1-432 <VAN>
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Cispecies: Halobacterium sp. NRC-1
Cispecies: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
Cispeciesion: G84373
Cispeciesion: G84373
Findy W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. US.A. 97, 12176-12181, 2000
Proc. Natl. Acad. Sci. US.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li*
A;Reference number: A84160; MUID:20504483; PMID:11016950
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                                      this accession replaces an interim accession for a sequence replaced by GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: trpS2
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
                                                                                                                                                                                                                                                                                                                                                  157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 DPDXTFIFQNSEF----TKIYEMAIPIAKKINFSMAKAVFGFTEQSKIGMIFFPAIQIAP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             227 EEDDK--KLKERYYACKONGELTGGECKRYLISKIOEFLKEHORRRKK-AEKLVEKFKYTG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158 DINKTFIFSDLDYMGMSSGFYKNVVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAP 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   218 SFSNSFPQIFRDRTDIQCLIPCAIDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQ 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDDDKLEQIRKDY---TSGAMLTGELKKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPR 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KYLWKDLTLDQAYGDAVE-NAKDIJACGFDINKTFIF---SDLDYM-GMSSGFYKNVVKI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 HRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDE
                                                                                                                                                                                                                                                                                                                                              99 MHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKYLWKD-LTLDQAYGDAVENAKDIIACGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278 TKMSASDPNSSIFLTDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 AEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGORPHHFLRRGIFFS
                                                                                                                                                                                                                                                                                                                                                                                     A,Note: this accession replaces an interim accession for a sequence C,Genetics:
A,Gene: PH1921
C,Keywords: aminoacyl-tRNA synthetase, ligase; protein biosynthesis
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                                                                                                                                                                                                            Length 301;
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                                                                                                                                                                                                        Query Match 29.6%; Score 626.5; DB 2; Best Local Similarity 44.2%; Pred. No. 5e-43; Matches 134; Conservative 56; Mismatches 92;
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          A; Experimental source: strain OT3
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A,Molecule type: DNA
A,Residues: 1-380 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Genetics:
A;Gene: trpS; PAB1111
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
                                                                                                                                                                                                                                 C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: C75020
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome
A;Reference number: A7501
A;Reference number: A7501
A;Reference prococcus abyssi genome sequence: insights into archaeal chromosome
A;Reference number: A7501
A;Reference number: DNA
A;Residues: 1-365 <KAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQDPYFRM 249
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                                                                                                                                                                                                            tryptophanyl-tRNA synthetase (trps) PAB1111 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 EDF-VDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIFFSH 70
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|: | : | |: | |: | |: | 346 IDKINNFLEEHR-RRREEAKELVHVFKYDGKLA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             342 KIQEFLKEHQKRRKKAEKQIEK 363
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- Methanobacterium thermoautotrophicum (strain Delta

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T43806

tryptophan-tRNA ligase (EC 6.1.1.2) [imported] - Encephalitozoon cuniculi (fragment)

c;Species Encephalitozoon cuniculi

c;Species 12-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004

C;Accession: T43806

C;Accession: T43806

E; Broussolle, V.; Peyret, P.; Metenier, G.; Gouy, M.; Vivares, C.P.

Mol. Biol. Evol. 15, 683-689, 1998

A;Title: Microsporidia, amitochondrial protists, possess a 70-kDa heat shock protein gene

A;Reference number: Z22693; MUID:98277683; PMID:9615449

A;Accession: T43806

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
                                                                                                        tryptophan-tRNA ligase (EC 6.1.1.2) - Methanobacterium thermoautotrophicum NiAlternate names: tryptophanyl-tRNA synthetase (C.Species: Methanobacterium thermoautotrophicum C.Species: Methanobacterium thermoautotrophicum C.Species: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
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A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A;Authors: Kaine, B.P.; Borodovsky, W.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A;Authors: F64476
A;Accession: F64476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q58810; GB:U67582; GB:L77117; NID:g1592064; PIDN:AAB99425.1; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Stārt codon: GTG
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
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                                                                                                                                                 213
                                                                                                                                                                                                                               NKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDD-KLEQIRKDYTSGAMLTGELK 361
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                                PYFRMTRDVAPRIGYP - - KPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKV
QKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQD
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                                                                                                                                                                                                                                                                                                                                                                                   Query Match 19.4%; Score 409.5; DB 2; Best Local Similarity 30.9%; Pred. No. 2.3e-25; Matches 119; Conservative 72; Mismatches 153;
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C. Accession: E69131
R. Sanith, D. R.; Doucette-Stamm, L. A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; I R.; Doucette-Stamm, L. A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; I i, Oiu, D.; Spadafora, R.; Vicaire, R.; Mang, Y.; Mierzbowski, J.; Gibson, R.; Jiwani, N.; Ki, S.; Church, G. M.; Daniels, C. J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J. N. J.; Bacteriol. 179, 7135-7155, 1997
A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct: A, Reference number: A69000; MUID:98037514; PMID:9371463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:026352; GB:AE000812; GB:AE000666; NID:92621298; PIDN:AAB8475;
A;Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: WTH251
X;Start codon: TTG
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14
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ECKNNTAEFIRKFFEELSVKREK 353
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Search completed: January 10, 2005, 21:23:46 Job time : 42 secs
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C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: O5-Dec-1997 #sequence_revision O5-Dec-1997 #text_change 09-Jul-2004
C;Accession: E69461
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
T; Pleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Uterbrack, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A;Rccession: E69461
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Accession: E69461
A;Scatus: 1-420 <a href="https://docs.nips.com/">A;Accession: Layouthor.oces.nips.com/</a>
A;Accession: E69461
A;Status: Uter Complete Grades: UNIPROT:028579; GB:AE000986; GB:AE000782; NID:g2689309; PIDN:AAB8955
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
             A;Cross-references: UNIPROT:096771; EMBL:AJ012470; PIDN:CAA10034.1
C;Superfamily: mammalian tryptophan-tRNA ligase; amino acid-tRNA ligase repeat homology
C;Keywords: ligase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVEIGGFAFIPPSSTYHRFTTGLTGG--KMSSSKPESYISLLDPPEEGAKKVMK-AFTGG 338
                                                                                                                                                                                                                                                                                  FSHRDMNQVLDAYENKKPFYLYTGRGPSSBAMHVGHLIPFIFTKWLQDVFNVPLVIQMTD 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311 RDTIEEHRQFGGNCDVDVSFMYLTFFLED-DDKLEQIRKDYTSGAMLTGELKKALIEVLQ 369
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                                                                                                                                                                                                                     15 VDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIFFSHRDMN 74
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                                                                                                                                                                                            12 EDFVDPWTVQTSSAK----GIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLRRGIF 67
                                                                                                                                                     Gaps
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                                                                                                          Length 134;
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                                                                                                                                                   35; Indels
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                                                                                                      th 18.2%; Score 386; DB 2; Similarity 51.5%; Pred. No. 4.4e-24; 68; Conservative 25; Mismatches 35;
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DEKFLWKSMRLE 134
A;Residues: 1-134 <PEY>
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                                                                                                      Query Match
Best Local S
Matches 68
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Swarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahi awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Ki DNA Res. 6, 83-101, 1999

A;Title: Complete ganome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrn A;Reference number: A72450; MUID:99310339; PMID:10382966

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A;Experimental source: strain Kl
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                                                                                                                                                                                                                                                                                                                           probable tryptophanyl-tRNA synthetase APE2461 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
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Vandekerckhove J.;
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Mol. Biol. (Mosk.) 30:319-329(1996),
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MEDLINE=93162043; PubMed=1286667;
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RMIM; 191050;
RM MIM; 191050;
RG; GO:0005625; C:soluble fraction; TAS.
RG; GO:0005625; C:soluble fraction; TAS.
RG; GO:0006412; P:protein biosynthesis; TAS.
RG; GO:0006436; P::ryptophany1-tRNA aminoacylation; TAS.
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RICEPPO; IPRO0130; TRNA-synt_1.
RICEPPO; IPRO0130; TRNA-synt_1.
REAM; PF00458; WHEP-TRS; 1.
REAM; PF00458; WHEP-TRS; 1.
RRS; RRICHS; RRG; RAS; 1.
RROSITE; PS00178; AA TRNA LIGASE_I; 1.
RROSITE; PS00178; AA TRNA LIGASE_I; 1.
RROSITE; PS00762; WHEP-TRS; 1.
RNA 3D-structure; Aminoacyl-tRNA synthetase; Rrotein biosynthesis.
RNA 3D-structure; Aminoacyl-tRNA synthetase; Protein biosynthesis.
RNA 3D-structure; Aminoacyl-tRNA synthetase; Protein biosynthesis.
RNA 3D-structure; Aminoacyl-tRNA synthetase; Rrotein biosynthesis.
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"KWSKS" region.
SY -> GD (in Ref. 3).
A -> R (in Ref. 4).
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                     EMBL; X67927; CAB94199.1; JOINED.
BMBL; X67928; CAB94199.1; JOINED.
PIR; A1633; A41706.
PDB; 1R6T; X-ray; A/B=1-471.
PDB; 1R6T; X-ray; A/B=4-471.
PDB; 1UH; X-ray; A/B=8-471.
Aarhus/Ghent-2DPAGE; 3524; IEF.
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVIQMTDDEKYLWKDLTLDQAYSYAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 360
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01-AUG-1992 (Rel. 22, Last sequence update)
05-AUL-2004 (Rel. 44, Last annotation update)
Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase)
                                                                                                                                 Plasmid pCMVSPORT 6.
Eukaryota, Metazoā, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 471;
                                                                              ğ
                                02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
Human full-length cDNA clone CSODMO04YH09 of Fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                    Li W.B., Gruber C., Jessee J., Polayes D.;
"Full-length cDNA libraries and normalization.";
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, SZ48006; CAD62335.1;
                                                                                                                                                                                                                                                                           Genoscope,
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             471 AA; 53165 MW; E96344449053A0D0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.3%; Score 2101; DB 2;
99.5%; Pred. No. 5.4e-160;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            475
                    Created)
                  02-MAR-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.5
Matches 399; Conservative
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                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                           TISSUE=Fetal liver;
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=Fetal liver;
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                              sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovinae; Bos.
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P17248;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
MEDLINE=91329348; PubMed=1907847;

Garret M., Pajot B., Trezeguet V., Labouesse J., Merle M.,
Gandar J.-C., Benedetto J.-P., Sallafranque M.-L., Alterio J.,
Gueguen M., Sarger C., Labouesse B., Bonnet J.,
"A mammalian tryptophanyl-tRNA synthetase shows little homology to prokaryotic synthetases but near identity with mammalian peptide chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R PIR; A40279; YWBO.

R HSSP, P07814; IFYJ.

R InterPro; IPR00306; S15/NS1_bind.

R InterPro; IPR001305; tRNA-synt_lb.

R InterPro; IPR001312; tRNA-synt_l.

R InterPro; IPR001312; tRNA-synt_l.

R InterPro; IPR000736; Trp_tRNA-synt_lb.

R Pfam; PF00579; TRNA-synt_lb; 1.

R Pfam; PF00139; TRNA-Synt_lb; 1.

R PIGNTS; PR01039; TRNA-SYNTHIRP.

R PROSITE; PS00178; AA TRNA_LIGASE I; 1.

R PROSITE; PS00178; AA TRNA_LIGASE I; 1.

R PROSITE; PS00178; AA TRNA_LIGASE I; 1.

R PROSITE; PS001762; WHEE TRS; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-tRNA(Trp).
-1- SUBUNIT: Homodimer.
-1- SIMILARITY: Belongs to class-I aminoscyl-tRNA synthetase family.
-1- SIMILARITY: Contains 1 WHEP-TRS domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
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"HIGH" region.
"KNSKS" region.
" A (in Ref. 2).
" F7E531750137EB32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        Garret M., Trezeguet V., Pajot B., Gandar J.-C., Merle M.,
Guegueiv M., Benedetto J.-P., Sarger C., Alteriot J., la Bouessec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Labouesse J., Bonnet J.;
Submitted (MAR-1990) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indela
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ilarity 95.8%; Pred. No. 3.6e-154;
Conservative 8; Mismatches 8;
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NCBI_TaxID=10090
                                                                                                                                                 Query Match
Best Local Simi:
Matches 367;
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                                                                                                                  SEQUENCE
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Q9DC65,
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                   VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRIDVQCLIPCA 314
                                                                 IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300
                                                                                                                                  KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 360
                                                                                                                                                     KVNKAAFSGGRDTVEEHRQFGGRCDVDVSFMYLTFFLEDDDKLEQIRRDYTSGAMLTGEL 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS TO 169-174 AND 227-228, AND FUNCTION.
MEDLINE=94009008; PubMed=8404867;
Prolova L.Y., Dalphin M.E., Justesen J., Powell R.J., Drugeon G.,
MCAUGHAIN K.K., Kisselev L.L., Tate W.P., Haenni A.-L.;
"Mammalian polypeptide chain release factor and tryptophanyl-tRNA synthetase are distinct proteins.";
EMBO J. 12:4013-4019(1993).
-!- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +
diphosphate + L-tryptophanyl-tRNA(Trp).
-!- SIMUNIT: Homodimer (By similarity).
-!- SIMULARITY: Contains I WHEP-TRS domain.
-!- SIMILARITY: Contains I WHEP-TRS domain.
-!- CATALYTION: Was originally (Ref.1) thought to be a eukaryotic release
                                                                                      IDQDPYFRWTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT
 VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=90239043; PubMed=2185472; MEDLINE=90239043; PubMed=2185472; Lee C.C., Craigen W.J., Muzny D.M., Harlow E., Caskey C.T.; Lee C.C., craigen W.J., amammalian peptide chain release factor "Cloning and expression of a mammalian peptide chain release factor "Cloning and expression of tryptophanyl-tRNA synthetases.";
                                                                                                                                                                                                                                                                                                                  SYW RABIT STANDARD; PRT; 475 AA.
P23512; Q28607;
01-NOV-1991 (Rel. 20, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
NCBI_TaxID=9986;
                                                                                                                                                                                                                     KKELIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSYDFQ 475
                                                                                                                                                                                                   KKALIEVLOPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          with sequence similarity to tryptophanyl-tRNA sy.
Proc. Natl. Acad. Sci. U.S.A. 87:3508-3512(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P07814; 1FYJ.

INTERPRO; IPR00968; S15/NS1_bind.

INTERPRO; IPR002305; FUNA-synt 1b.

INTERPRO; IPR001412; FUNA-synt_I.

INTERPRO; IPR002306; Trp FRNA-synt_I.

INTERPRO; IPR002306; Trp FRNA-synt_I.

INTERPRO; IPR000738; WHEP-TRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; W33460; AAA31246.1; ALT_SEQ.
EMBL; U02595; AAB60257.1; -.
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Pfam; PF00579; tRNA-synt lb; 1. Pfam; PF00458; WHEP-TRS; 1. PRINTS; PR01039; TRNASYNTHTRP.

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120
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                                                                                                                                                                                                                                                                                                                                                                                                        FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFDVP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255 VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFHGQADIQCLIPCA 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYSSGAMLTGEL 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last amountation update)
Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
clone:1200002C07 product:tryptophanyl-tRNA synthetase, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 NHG-PDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH
                                                                                                                                                                                                                                                                                                                                                                           FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP
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TIGREAMS; TIGRO0233; trpS; 1.

PROSITE; PS00178; AA TRNA LIGASE_I; 1.

PROSITE; PS00762; WHEE TRS; 1.

Aminoacyl-trnA synthetase; ATP-binding; Ligase; Protein biosynthesis.

SITE 168 177 "HIGH" region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                              DB 1; Length
                                                                                                                                                                                                                                           Indels
                                                                                     23 68 WHEP-TRS.
168 177 "HIGH" region.
353 357 "KWSKS" region.
475 AA; 53799 WW; 33BC9E718FF45DC4 CRC64;
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                                                                                                                                                                                                                                                13;
                                                                                                                                                                                              92.7%; Score 1961.5; DB 1; ilarity 91.5%; Pred. No. 8.6e-149; Conservative 20; Mismatches 13;
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STRAIN=C57BL/6J; TISSUE-Lung;
MEDLINE=99279253; PubMed=10349636;
Carrinci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=21085660; PubMed=11217851;
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VIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKNV 181

122

182

242 316 302

196 VIQMSDDEKYLWKDLTLEQAYSYTVENAKDIIACGFDINKTFIFSDLEYMGQSPGFYRNV

VKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAI 241

256 VKIQKHVTFNQVKGIFGFTDSDCIGKISFPAVQAAPSFSNSFPKIFRDRTDIQCLIPCAI

315

DODPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKWSASDPNSSIFLTDTAKQIKTK 301

316 VNKAAPSGGRDTVEEHRQFGGNCEVDVSFMYLTFFLEDDDRLEQIRKDYTSGAMLTGELK 435

KALIEVLOPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 401

362

VNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELK 361

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A Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
A Arakwa T., Bono H., Carninch P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishii K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Muramatsu M., Hayashizaki Y.,
L Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
R EMBL, AKO04541; BAB233571; -.
                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUB=Lung;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630 (2000).
                                   the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                      STRAIN-C57BL/64); TISSUE-Lung;
MEDLINE-20530913; PubMed=11076861;
Shibata K., Itoh M., Alzawa K., Naggoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Alzawa K., Naggoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara B., Watshiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watshiki M., Ohazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rikik integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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GO; GO:000524; F:ATP binding; IEA.
GO; GO:0004830; F:Lryptophan-tRNA ligase activity; IEA.
GO; GO:0004836; P:tryptophan-tRNA ligase activity; IEA.
GO; GO:0006485; P:tryptophan-tRNA aminoacylation; IEA.
InterPro; IPR003069; S15/NS1_bind.
InterPro; IPR001412; tRNA-synt_1b.
InterPro; IPR001412; tRNA-synt_1.
InterPro; IPR001306; Trp_tRNA-synt_1b.
InterPro; IPR002306; Trp_tRNA-synt_1b.
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TIGREPAGE; TGRO0233; LTPS; 1.
PROSITE; PS00178; AA TRNA LIGASE_I; 1.
PROSITE; PS00762; WHEP_TRS; 1.
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Pfam; PF00458; WHEP-TRS; 1.
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  STRAIN=C57BL/6J; TISSUE=Lung;
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RESTRAIN=NRRI; TISUE-Mammary tumor. WAP-Tag model. 5 months old;

KENDINE=22388257; PubMed=12477932;

KIGURENE: Collins F.S., Magner L., Derge J.G.,

KIGURES R.D., Collins F.S., Magner L., Schemen C.M., Schuler G.D.,

KIGURENER R.P., Collins F.S., Magner L., Schemen C.M., Schuler G.D.,

Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altechul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RA HOPKINS R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

RA Diatchenko L., Marusina K., Farmer A.P., Rabin G.M., Hong L.,

RA Barbers M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glubs R.A.,

Rahey J., Helton E., Ketteman M., Rodan A., Rodrigues S., Sanchez A.,

Rahes J., Helton E., Ketteman M., Green E.D., Dickson M.C.,

Rahes J., Marra M., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Marra M.A.;

Jones S.J., Marra M.A.;

A Jones S.J., Marra M.A.;

RA Feber S. Marra M.A.;

RA Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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STRAIN=NWRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004830; F:LYTyptophan-tRNA ligase activity; IEA.
GO; GO:0006436; P:LYTyptophanyl-tRNA aminoacylation; IEA.
InterPro; IPR009068; S15/NS1_bind.
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436 KTLIDVLQPLIAEHQARRKAVTEETVKEFMTPRQLSFHFQ 475
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Submitted (FEB-2001) to the
EMBL; BC003450; AAH03450.1;
                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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62 LRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPL 121

NHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHF

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Best Loca Matches

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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNKHAFSGGRDTVEEHRQFGGNCEVDVSFMYLTFFLEDDDRLEQIRKDYTSGAMLTGELK 435
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STRAIN-C57BL/6; TISSUE-Brain;
STRAIN-C57BL/6; TISSUE-Brain;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Brownstein M.J., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                           VKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAI
                                                                                                                                                                                                                                         NHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHF
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                                                                                                                                                                                  92.5%; Score 1957; DB 2; Length 481; 91.5%; Pred. No. 2e-148; ive 20; Mismatches 14; Indels (
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Last sequence update)
Last annotation update)
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InterPro; IPR002305; tRNA-synt_1b.
InterPro; IPR001412; tRNA-synt_1.
InterPro; IPR002306; Trp_tRNA-synt_1b.
InterPro; IPR000738; WHEP-TRS.
Pfam; PF00579; tRNA-synt_1b; 1.
Pfam; PF00458; WHEP-TRS; 1.
PR01TS; PR01039; TRNASYNTHTR.
TIGRRAMS; TIGR00233; trpS; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_1; 1.
PROSITE; PS00763; WHEP-TRS; 1.
PROSITE; PS00762; WHEP-TRS; 1.
SEQUENCE 481 AA; 54325 MW; A754EIDDF
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Matches 366; Conservative
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0802Y4
0802Y4
AC 0802
DT 01-JT
DT 01-JT
DT 01-JT
DT 01-Mars
GN Wars
GN Wars
CO Euka
OC Euka
OC Euka
CO RURA
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RN (1]
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RN KA SEQU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 LRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VNKHAFSGGRDTVEEHRQFGGNCEVDVSFMYLTFFLEDDDRLEQIRKDYTSGAMLTGELK 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTK 301
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalaka U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 VIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKNV
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                                                                                                                                                                                                                                                                                                                                                                                                    Straubberg R.;
Straubberg R.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC046232; AAH46232.1; -.
HSSP; BO7814; ITVJ.
MGD; MGI:104630; Wars.
GO; GO:0006324; F:ATP binding; IEA.
GO; GO:0006436; F:ATP binding; IEA.
GO; GO:0006436; F:ATP binding; IEA.
GO; GO:0006436; F:ATP binding; IEA.
GO; GO:0006436; F:ATP binding; IEA.
InterPro; IPR00306; S15/Nal_bind.
InterPro; IPR00306; TRNA-Synt_I.
InterPro; IPR00306; TRP tRNA-Synt_I.
InterPro; IPR00306; TRP tRNA-Synt_I.
InterPro; IPR00308; WHEP-TRS.
FEam; PF00459; WHEP-TRS; I.
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                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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(Rel. 27, Last sequence update)
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TIGREAMS; TIGR00233; LTDS; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
PROSITE; PS00762; WHEP_TRS; 1.
SEQUENCE 475 AA; S3613 WW; D841D8B5
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                           cDNA sequences.",
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316 DQDPYFRMTRDVAPRIGHPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKSK 375
                                                                                                                                                                                             242 DQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTK 301
                                                                                                                                                                             VNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELK 361
                                                                                 VIQMTDDEKYLWKDLTLDQAYGDAVENAKDIJACGFDINKTFIFSDLDYMGMSSGFYKNV
                                                                 VKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klein S.L., Strausberg R.L., Wagner L., Pontlus J., Clifton S.W., Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                      362 KALIEVLOPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                       475
                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                  Created)
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MEDLINE=22341132; PubMed=12454917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dev. Dyn. 225:384-391(2002).
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mouse cDNA sequences.
                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klein S., Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopodinae; Xenopus.
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                             MGC81110 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                        Name=MGC81110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      initiative.
                                                                   182
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R MGD; MGI: J04630; Wars.

R InterPro; JPR002306; ENA-synt_lb.

R InterPro; JPR002306; TRNA-synt_lb.

R InterPro; JPR002306; TrD tRNA-synt_l.

R InterPro; JPR000738; WHEP-TRS;

R Pfam; PF000739; TRNA-synt_lb.

R Pfam; PF000459; WHEP-TRS; 1.

R PRINTS; PR01039; TRNASYNTHTRP.

R PROSITE; PS00179; ANNA LIGASE_I; 1.

R PROSITE; PS00176; WHEP_TRS; 1.

R PROSITE; PS00176; WHEP_TRS; 1.

R PROSITE; PS00176; WHEP_TRS; 1.

R Alternative splicing; Aminoacyl-tRNA synthetase; ATP-binding; Ligase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCDSDATKASEDFVDPWTVRTSSAKGIDYDKLIVQPGSSKIDKELINRIERATGQRPHRF 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 NHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHF
                                                                                                                      MEDLINE=95018226; PubMed=7932716;

MEDLINE=95018226; PubMed=7932716;

Pajot B., Sarger C., Bonnet J., Garret M.;

Pajot B., Sarger C., Bonnet J., Garret M.;

An alternative splicing modifies the Crerminal end of tryptophanyl-tRNA synthetase in murine embryonic stem cells.";

J. Mol. Biol. 242:599-603(1994).

-!- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP + diphosphate + L-tryptophanyl-tRNA(Trp).

-!- SUBUNIT: Homodimer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                     found only in embryonic stem cells. SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family. SIMILARITY: Contains I WHEP-TRS domain.
                                                                                                                                                                                                                                                               Event-Alternative splicing; Named isoforms=2;
Name=1; Synonyms=Long;
Isoid=p3291-1; Sequence=Displayed;
Name=2; Synonyms=Short;
Isoid=p32921-2; Sequence=VSP 006313;
TISSUE SPECIFICITY: Isoform 2 is widely expressed, isoform 1 is
05-JUL-2004 (Rel. 44, Last annotation update)
Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
                                                      Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B05A452C08074F52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "HIGH" region.
"KMSKS" region.
Missing (in isoform 2).
/FTId=VSP_006313.
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EMBL; X69657; CAA49348.1; -.
PIR; S50053; S50053.
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Best Local Similarity 90.8
Matches 363; Conservative
                                        Name=Wars; Synonyms=WRS;
                                                                                                                                                                                                                                                      ALTERNATIVE PRODUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68
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                                                                                              NCBI_TaxID=10090;
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353
476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLRRGIFFSHRDMHQVLDAYENKKPFYLYTGRGPSSEALHVGHLIPFIFTKWLQEVFNVP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDQDPYFRMTRDVAPRINYPKPALMHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKN 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 360
                                                                                                                                                                                                                                                                                                                                                                                                                            1 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
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Kenopus laevis (African clawed frog).

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibla; Barrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  research: The NIH Xenopus
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                                                                                                                                                                                                                                                                                                                      Length 475;
                                                                                                                                                                                                                                                                                                                                                             Indels
  Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                          761EF9EA4B754F71 CRC64;
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14-APR-2004 (TrEMBLrel. 27, Last sequence update)
14-APR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKALIEVLOPLIAEHQARRKEVTDEIVKEFMTPRKLSFDF
                                                                                                                                                                                                                                                                                                               87.1%; Score 1844; DB 2;
83.8%; Pred. No. 2.3e-139;
ive 44; Mismatches 21;
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                 EMBL; BC068695; AAH68695.1; -...
INCEPTO; IRRO90668; S15./NS1 bind.
INCEPTO; IRRO02305; LRNA-8ynt_1b.
INCEPTO; IRRO02305; LRNA-8ynt_1b.
INCEPTO; IRRO02306; TYP_LRNA-8ynt_1b.
INCEPTO; IRRO02306; TYP_LRNA-8ynt_1b.
Fam; PF00579; LRNA-8ynt_1b; 1.
Pfam; PF00579; WHEP-TRS; 1.
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                                                                                                                                                                                     PRINTS; PRO1039; TRNASYNTHTRP.
TIGRRPMs; TIGRO0233; LTDS; 1.
PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
PROSITE; PS00762; WHEP_TRS; 1.
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Dev. Dyn. 225:384-391(2002)
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Klausner R.D., Celling F.S., Wagner L.H., Derge J.G.,
Rlausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A both of the colling R., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Caavanic T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McZwan P.J., McKernan R.J., Malek J.A., Gunazane P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
T. "Generation and initial analysis of more than 15,000 full-length human
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Submitted (APR.2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC068695; A4468695.1; -.
Hypothetical protein.
SEQUENCE 475 AA; 53856 MW; 761EF9EA4B754F71 CRC64;
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Last annotation update)
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llarity 83.8%; Pred. No. 2.3e-139;
Conservative 44; Mismatches 21;
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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  Anura; Mesobatrachia; Pipoidea; Pipidae;
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC046713; AAH46713.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004830; F:LTYDtOphan-tRNA ligase activity; IEA.
GO; GO:0006436; P:LTYDtOphanyl-tRNA aminoacylation; IEA.
InterPro; IPR002068; S15/NS1_bind.
InterPro; IPR00205; tRNA-8ynt_lb.
InterPro; IPR001412; tRNA-8ynt_l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.
1: CDCCE6EDB08AE357 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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; Pred. No. 2e-137;
39; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO1039; TRNASYNTHTRP.
TIGRRPMS; TIGRO0233; LTPS; 1.
PROSTIE; PS00178; AA TRNA LIGASE I; 1.
PROSTIE; PS00762; WHEP TRS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002306; Trp tRNA-Synt_lb.
InterPro; IPR000738; WHEP-TRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22341132; PubMed=12454917;
                                                                                                                                  MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00579; tRNA-synt_lb; 1.
Pfam; PF00458; WHEP-TRS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53830 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.0%;
83.2%;
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Best Local Similarity 83.24
Matches 333; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.
Amphibia, Batrachia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P07814; 1FYJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      475 AA;
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                                                                                        SEQUENCE FROM N.A.
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                       Xenopodinae; Xenk
NCBL_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "ISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FISSUE=Embryo;
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                                                                                                                                                                                                                                                                                                                                     316 IDQDPYFRMTRDVAPRINYPKPALMHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKS 375
                                                                                                                                                                                                                                                                                     241 IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196 LVVQLTDDEKYLWKDLTLEKAYQYATENAKDIIACGFDVNKTFIFSDLEYMGKSSGFYQN 255
                                                                                                                                             181 VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae, Rattus.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              379 AA.
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PROSITE; PSO0178; AA_TRNA_LIGASE_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR002305; tRNA-synt_1b.
Interpro; IPR001412; tRNA-synt_I.
Interpro; IPR003306; Trp_tRNA-synt_1b.
Pfam; PP00579; tRNA-synt_1b; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
Hypothetical protein.
Rattus norvegicus (Rat).
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SEQUENCE 379 AA; 4
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TISSUE-Production N. A.

TISSUE-Production N. A.

MEDLINE=2238257; Pubbled=12477932;

MEDLINE=2238257; Pubbled=12477932;

MALacusberg R. L., Feingold E. A., Grouse L. H., Derge J.G., Schuler G.D.,

M. Klausner R. D., Colling F. S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S. F., Zeeberg B. Buetow K. H., Schaefer C.F., Bhat N. K.,

Diatchenko L., Marusina K., Farmer A. A., Rubin G.M., Hong L.,

Diatchenko L., Marusina K., Farmer A. A., Rubin G.M., Hong D.,

R. Diatchenko L., Marusina K., Farmer A. A., Rubin G.M., Hong D.,

Roalecon M., Soares M. B., Bonaldo M. F., Casavant T. L., Scheetz T. E.,

Roalecon M., Joanes M. P. Toshiyuki S., Abramson R. D., Mullahy S.J.,

Raha S. S., Morwan P. J., McKernan K. J., Marek J. A., Gunarane P. H.,

Richards S., Worley K.C., Hale S., Garcia A. M., Gaby L.J., Hulyk S. W.,

Millalon D. K., Muray D. M., Sodergren B. J., Lu X., Gibbs R. A.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J. E.,

M. Generation and initial analysis of more than 15,000 full-length human
                                                                  VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA 240
                                                                                                                                                                                                       IDODPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300
                                                                                                                                                                                                                                                                           120
                                                                                                                  LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 180
            83
FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus
                                                                                                                                                                                                                                                                                                                                         301 KVNKHAFSGGRDTIEEHROFGGNCDVDVSFMYLTFFLEDDDKLEQIRK 348
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SEGUENCE 379 AA; 42880 MW; B9CDB2248780C2E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-WAR-2004 (TrEMBLrel. 27, Created)
02-WAR-2004 (TrEMBLrel. 27, Last sequence update)
02-WAR-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mouse cDNA sequences."
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AAH61752;
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AAH61752
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Length 379;

81.9%; Score 1734; DB 2; 92.2%; Pred. No. 1.2e-130;

Query Match Best Local Similarity

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                                                                                       LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKN 180
                                                     61 FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP 120
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                                                                                                                            30 SNGDPDATKASEDFVDPWTVRTSSAKGIDYDKLIVQFGSSKIDKELINRIERATGQRPHR
                                                                                                                                                               241 IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT
                   1 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGGRPHH
                                                                                                                                                                                                                                                                                                               Exachydanio (Zebrafish) (Danio rerio).
Brachydanio rezio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBL_TaxID=7955;
 Gaps
 ó
                                                                                                                                                                                                   301 KVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLIFFLEDDDKLEQIRK 348
                                                                                                                                                                                                            Strausberg R.;
Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC059603; AAH596031; -.
InterPro; IPR009068; S15/NS1 bind.
InterPro; IPR002305; tRNA-synt_lb.
 10; Indels
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                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
 321; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                  463 AA
                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created)
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STRAIN=Wild_type; TISSUE=Eye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA sequences.
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MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Strausberg R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Browstein M.J., Wedwan P.J., McKernan K.J., Abramon R.D., Mullahy S.J.,

Bosak S.S., Loquellano N.A., Peters G.J., Abramon R.D., Mullahy S.J.,

Bosak S.S., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             FFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMT
                                                                                                                                                                                                                                                                                                                                                     ATEAEEDFVDPWTVQTSSAKGIDYDK1,IVRFGSSKIDKELINRIERATGQRPHHFLRRGI
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes,
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                                                                                                                                                                                                                                                            Length 463;
                                                                                                                                                                                                                                                       $; Score 1734; DB 2; Length 4
8; Pred. No. 1.5e-130;
42; Mismatches 30; Indels
InterPro; IPR001412; tRNA-synt_I.
InterPro; IPR002306; Trp_tRNA-synt_lb.
InterPro; IPR000738; WHEP-TRS.
Pfam; PF00458; WHEP-TRS.
Pfam; PF00458; WHEP-TRS; I.
PRINTS; PR01039; TRNASYNTHTRP.
TIGREAMS; TIGR0233; trpS; I.
PROSITE; PS00178; ATRNA_LIGASE_I; I.
PROSITE; PS00178; ATRNA_LIGASE_I; I.
SEQUENCE 463 AA; 52372 MW; ED406A47C9628FEF CRC64;
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24-MAY-2004 (TrEMBLrel. 27, Last sequence update)
24-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein zgc:73274.
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81.6%;
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les 320; Conservative
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Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFGDRKDVQCLIPCAIDQDPY
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Submitted (OCT-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-2003)
Submitted PEO59603, AMP59603.1;
Hypothetical protein.
SEQUENCE 463 AA; 52372 MW; ED406A47C9628FEF CRC64;
                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 81.9%; Score 1734; DB 2; Best Local Similarity 81.6%; Pred. No. 1.5e-130; Matches 320; Conservative 42; Mismatches 30;
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ORGANISM: Homo sapiens
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Sequence 45650, A
Sequence 61162, A
Sequence 19803, A
Sequence 19803, A
Sequence 4201, Ap
Sequence 5765, App
Sequence 2, Appli
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Sequence 4392, Ap
Sequence 5784, Ap
Sequence 3, Appli
Sequence 2, Appli
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857, App
18205, A
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4257, Ap
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3686, Ap
28, Appl
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                                                                                                  January 10, 2005, 21:16:34; Search time 40 Seconds (without alignments) 664.838 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
               version 5.1.6
- 2005 Compugen Ltd.
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US-08-270-767-45550

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US-09-248-796A-19803

US-09-248-796A-19803

US-09-248-796A-19803

US-09-248-796A-19803

US-09-248-796A-19803

US-09-107-532A-5765

US-09-425-666-2

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US-09-425-666-2

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US-09-134-000C-5784

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US-09-134-010A-39

US-09-138-452A-857

US-09-123-615-4

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US-09-134-00C-3686

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US-08-134-00C-3686

US-08-35-990-28
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993
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seq length: 200000000
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Issued
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Perfect score:
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Maximum DB
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No.
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Sequence 163, Application US/09919039
Patent No. 6727066
GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
TITLE OF INVENTION: GENES US/09/919,039
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT PILING DATE: 2002-09-09
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL PROGRAM
SEQ ID NO 163
LENGTH: 471
                                Sequence 4, Appli
Sequence 1676, A
Sequence 1676, A
Sequence 1820, Appl
Sequence 1820, Appl
Sequence 1811, Appl
Sequence 1874, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 22, Appli
Sequence 426, Appli
Sequence 1246, Appli
Sequence 2554, Appli
Sequence 2554, Appli
Sequence 8, Appli
Sequence 8, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLRRGIPFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGPDINKTFIFSDLDYMGMSSGFYKN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KVNKHAPSGGRDTIEEHROFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 430
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   Sequence Sequence Sequence S
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US-08-928-100-4
US-09-183-134-2
US-09-492-581-4
US-09-425-666-4
US-09-248-796A-17676
US-09-134-001C-5141
US-09-134-001C-5141
US-09-134-001C-5141
US-09-3489-039A-10919
US-09-3489-039A-10919
US-09-383-12
US-09-391-3466
US-09-134-001C-4701
US-09-134-001C-4701
US-09-134-001C-4701
US-09-134-001C-4701
US-09-391-340-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6727066 2705515CD1
US-09-919-039-163
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amino acid
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Patent No. 6174713

GENERAL INFORMATION:

APPLICANT: Houman, Fariba

TITLE OF INVENTION: CANDIDA CYTOPLASMIC TRYPTOPHANYL-TRNA

TITLE OF INVENTION: SAME

TITLE OF INVENTION: SAME

CORRESPONDENCE: 26

CORRESPONDENCE: 26

CORRESPONDENCE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 FFSHRDLHTILTLREQGKPFYLYTGRGPSSGSLHVGHLVPFIMTKWLQETFDVPLVIQLT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEKTLWKDLKVEDAIKLGRENAKDIVAIGFDVNKTFIFNNLEFVGKCPAMYQNIIRIQK 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGFYKNVVKIQK 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKHA 306
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                                                                                                    Sequence 45650, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 45650
LENGTH: 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMT
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 61.0%; Score 1290.5; DB 4; Length Best Local Similarity 67.4%; Pred. No. 3.6e-136; Matches 240; Conservative 51; Mismatches 64; Indels
                         KKALIEVLOPLIAEHOARRKEVTDEIVKEFMTPRKLSFDFQ 471
                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-45650
                                                                                                                                                                                                                                                                                                                                            ORGANISM: Drosophila melanogaster
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                                                                                  RESULT 2
US-09-270-767-45650
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US-08-876-885-26
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251 QDPYFRVCRDVADKLRFTKPALIHAKFFPALQGASTKMSASDTTTSIFMGDTAKQIQKKI 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCAID 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Mucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Mucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 61162
LENGTH: 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 RGIFFSHRDMNQVLDAYENKKFFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 TEAEEDFVDPWTVQ----TSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHHFLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; Length 424;
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/876,885
FILING DATE: 16-UUN-1997
CLASSIFICATION: 435
ATTORNEY/AGBNT INFORMATION:
NAME: Brook, David E.
REFERRATION NUMBER: 22,592
REFERRATION NUMBER: CP197-02
TELEPONE: (781) 861-9540
TELEPAK: (781) 861-9540
TELEPAK: (781) 861-9540
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.6%; Score 1218.5; DB 3;
57.1%; Pred. No. 5e-128;
iive 71; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                363 ALIEVLOPLIAEHQARRKEVTDEIVKEFMTPRKLSF 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   371 ECÍTVLÓEFVSAYÓEŘŘSKÝDDOVVEKFMKPHKLVF 406
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Matches 226; Conservative
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Sequence 7201, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:
TTPLICANT: Gary L. Breton et al.
TTPLICANT: Gary L. Breton et al.
TTPLIC OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04

NOWHEND OF SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              319 QFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELKKALIEVLQPLIAEHQAR 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              259 YPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKTKVNKHAFSGGRDŢIEEHR
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                              FOR DIAGNOSTICS AND THERAPEUTICS
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9.2%; Score 195; DB 4; L
Best Local Similarity 25.9%; Pred. No. 5.1e-13;
Matches 84; Conservative 56; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 550; DB 4;
Pred. No. 2.7e-53;
TITLE OF INVENTION: FOR DIAGNOSTICS AND THEKLE PILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 19802
LENGTH: 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 RSKVDDQVVEKFMKPHKLVF 195
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US-09-328-352-4201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 106; Conservative
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Best Local Similarity
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCES RELATING TO CANDIDA ALBICAN
                                                                                                                                                                 ä
                                                                                                                                                                                                                                                                                                                                                                                                    213 IQAAPSFSNSFPQIFRDRTDIQCLIPCAIDQDPYFRMTRDVAPRIGYPKPALLHSTFFPA 272
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                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                 153 IACGFDINKTFIFSDLDYMGMSSGFYKNVVKIQKHVTFNQVKGIFGFTDSDCIGKISFPA
                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                DB 4; Length 210;
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                                                                                                                                                              32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KALLAN Weinstock et al TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES; TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS FILE REPERBUCE: 107196.132; CURRENT APPLICATION NUMBER: US/09/248,796A; CURRENT FILING DATE: 1999-02-12; PRIOR APPLICATION NUMBER: US 60/074,725; PRIOR APPLICATION NUMBER: US 60/096,409; PRIOR FILING DATE: 1998-02-13; PRIOR APPLICATION NUMBER: US 60/096,409; PRIOR FILING DATE: 1998-08-13; NUMBER OF SEQ ID NOS: 28208; SEQ ID NO 19803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.3%; Score 684.5; DB 4, 55.8%; Pred. No. 2.6e-68; tive 42; Mismatches 50
                                                                                                36.6%; Score 774.5; DB 4 68.6%; Pred. No. 1.4e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | |||||| ||||::| |: | |||||:||
LKFFLEDDAKLEEVRVAYSKGEMLTGEIKK 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTFFLEDDDKLEQIRKDYTSGAMLTGELKK 362
                                                                                                                                                              33; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 19803, Application US/09248796A; Patent No. 6747137; GENERAL INFORMATION:
                                                                                            Query Match
Best Local Similarity 68.61
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Candida albicans
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Matches 125; Conservative
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US-09-248-796A-19803
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                              US-09-270-767-61162
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84 KPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKY-LWKDLTLDQAY 142
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                                                                                                                                                                                                  225 PADVLQKKV----MSMYTDPNHIHVQDPGQVEGNMVFTYLDVFGTDKEAIEEMKAHYRRG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 --FNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQC-LIPCAIDQDPY 246
                                        ----DITAFKANLVPVGEDOKPM 169
                                                                                                                 247 FRMTRD------VAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTD
                                                                                                                                                                         294 TAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFWYLTFFLEDDDKLEQIRKDYTSG
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Similarity 24.0%; Pred. No. 6.1e-12;
31; Conservative 60; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NATA:
CLASSIPICATION NATA:
CLASSIPICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9619072.3
FILING DATE: 12-SEP-1996
ATTOR APPLICATION DATA:
APPLICATION NUMBER: 9619072.3
FILING DATE: 12-SEP-1996
ATTOR APPLICATION NUMBER: 9818
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P31624-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                      354 AMLTGELKKALIEVLOPLIAEHOARRKEV 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gentry, Danile
APPLICANT: Greenwood, Claire
APPLICANT: Lawlor, Elizabeth
ITLE OF INVENTION: NO. 6046174el trpS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                             126 TEIEQKK----FGESVPTGFFIYPVSQAA-
                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/08928100
; Patent No. 6046174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPALIDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 341 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 GDAVEN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: PA
COUNTRY: USA
ZIP: 19406-0939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM COM
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Simi
Matches 81;
                                                                                                                                                                                                                                                                                                                                                                                                   US-08-928-100-2
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                                                                                                                                                                                                                                                                    Sequence 5765, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 NPEKVSSNVLQVALDYLAVGLDPAKSTLFIQSQIPELARLIMYYLNLVSVGRVRRNPTVK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 LYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKYLWKDLTLDQAYGDAVE 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 N------AKDIIACGFDINKT--FIFSDLDYMGMSSGFYKNVV---KIQKHVT-- 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VNKHAFSGGRDTIEEHROFGGNCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELK 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
8.8%; Score 186; DB 4; Length 348;
Best Local Similarity 24.9%; Pred. No. 5.5e-12;
Matches 82; Conservative 57; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature; SEQUENCE: SEQUENCE DESCRIPTION: SEQ ID NO: 5765: US-09-107-532A-5765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Enterococcus faecium
                                                                                                                                              280 KRLEGVLKELITPIRERREELAKD 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: <Unknown>
                                                                                                                     362 KALIEVLOPLIAEHOARRKEVTDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 348 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 5765:
                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                    US-09-107-532A-5765
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213 LADDADTLRKKVMSMYTDPDHIRVEDPGKIEGN----WVFHYLDVFGRPEDAQEIADMKE 268
                                                                     245 PYFRMTRD------VAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIF 290
                                                                                                                                                                                                                                                     157 PMIEQTREIVRSFNNAYNCDVLVEPEGIYPENE--RAGRLPGLDG-NAKMSKS-LNNGIY 212
                                                                                                                                                                                                                                                                                                    291 LIDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFF--LEDDDKLEQIRK 348
                                          143 GDAVEN-----AKDIIACGFDINKTFIF--SDLDYMGMSSGFYKNVV---KIQK 186
                                                                                                                               187 HVTFNQVKGIFGFTDSDCIGKISFPAIQAA--PSFSNSFPQIFRDRTDIQCLIPCAIDQD 244
  ----VLLQEEDKYDMFVFLADQQAL 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                 269 RYQRGGLGDVKTKRYLLEILERELGPIRERRIEFAKDM 306
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8.8%; Score 185.5; DB 4;
Best Local Similarity 24.0%; Pred. No. 6.1e-12;
Matches 81; Conservative 60; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09425666
Patent No. 6446976
GENERAL INFORMATION:
APPLICANT: Generacod, Claire
APPLICANT: Greenwood, Claire
APPLICANT: Lawlor, Blizabeth
TITLE OF INVENTION: No. 6416976el trpS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedaland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FASEES for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/425.666
  3 KPIIL-TGDRPTGK-LHIGHYVGSLKNR---
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/928,100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNAY AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P316
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 341 amino acida
TYPE: amino acid
STRANDEDNESS: gingle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 341 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , TOPOLOGY: linear
, MOLECULE TYPE: protein
US-09-425-666-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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                                                                  ---VAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIF 290
                                                                                                                                                                                                               LTDTAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFF--LEDDDKLEQIRK 348
                                                                                                                                                                                                                                            213 LADDADTLRKKVMSMYTDPDHIRVEDPGKIEGN----MVFHYLDVFGRPEDAQEIADMKE 268
50 TDHAKDPQTIVESIGNVALDYLAVGLDPNKSTIFIQSQIPELAELSMYYMNLVSLARLER 109
                                        187 HVTFNQVKGIFGFTDSDCIGKISFPAIQAA--PSFSNSFPQIFRDRTDIQCLIPCAIDQD 244
                                                                                                                                                                    157 PMIEQTREIVRSFNNAYNCDVLVEPEGIYPENE--RAGRLPGLDG-NAKMSKS-LNNGIY 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 KPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVPLVIQMTDDEKY-LWKDLTLDQAY
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8.8%; Score 185.5; DB 3; Length 341;
Best Local Similarity 24.0%; Pred. No. 6.1e-12;
Matches 81; Conservative 60; Mismatches 128; Indels 69
                                                                                                                                                                                                                                                                                                                            269 RYQRGGLGDVKTKRYLLEILERELGPIRERRIEFAKDM 306
                                                                                                                                                                                                                                                                                                 349 DYTSGAMLTGELKKALIEVLQPLIAEHQARRKEVTDEI 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gentry, Danile
APPLICANT: Greenwood, Claire
APPLICANT: Lawlor, Elizabeth
TITLE OF INVENTION: No. 6346409el trpS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: SMithKline Beecham Corporation
STRETT: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FASTEM: DOS SOFTWARE: FASTED for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/492,581 FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRICAL APPLICATION DATA:
APPLICATION NUMBER: US/08/928,100
FILING DATE: 12-SEP-1997
APPLICATION NUMBER: 9619072.3
FILING DATE: 12-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P31624-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----
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Patent No. 6346409
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 341 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 610-270-5090
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                                                                                                                          245 PYFRMTRD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-492-581-2
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APPLICANT: LYND Doucette-Stamm et al
APPLICANT: LYND Doucette-Stamm et al
APPLICANT: LYND Doucette-Stamm et al
APPLICANT: LYND Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTERCOCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE APPLICATION NUMBER: US/09/134,000C
CURRENT APPLICATION NUMBER: US 60/055,778
PRIOR PLING DATE: 1997-08-15
NUMBER: OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NO 5784
LENGTH: 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 -----NPEKVSANVLEVALDYLAVGLDPTKTTIFIQSQIPQLAELTMYYLNLVTTSRVRR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 LWKDLTLDQAYGDAVENAKDIIACGFDINKTFIF--SDLDYMGMSSGFYKNVV---KIQK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187 HVT----FNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQC-LIPCAI 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 NPTVKABIBOKK----FGEGVPTGFFIYPVSOAA-------DITAFOANLVPVGE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 DQDPYFRMTRD------VAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSS 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOKPMLEQAQEIVHSFNQTYGEVLVRPEAVLPPKGMGR---LPGIDG-NGKMSKSLGN-G 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  289 IFLIDIAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFFLEDDDKLEQIRK 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 39, Application US/08743130A
Sequence 39, Application US/08743130A
Sequence 39, Application US/08743130A
Sequence 30, Application
Sequence 30, Application
Septicant: Sassanfar, Mandana
APPLICANT: Shen, Xiaoyu
APPLICANT: Tao, Nianjun
APPLICANT: Tao, Jianshi
APPLICANT: Tao, Jianshi
APPLICANT: Tao, Jianshi
APPLICANT: Tao, Jianshi
APPLICANT: Tao, Jianshi
APPLICANT: Houman, Fariba
TITLE OF INVENTION: CANDIDA TYROSYL-tRNA SYNTHETASE
TITLE OF INVENTION: PROTEINS, NUCLEIC ACIDS AND STRAINS COMPRISING SAME
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 LYTGRGPSSEAMHVGHLIP------FIFTKWLQDVFNVPLVIQMTDDEKY 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : || |: : :|:|| : :|| |: : || |: : :|:|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: : :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :|| |: :| 
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8.2%; Score 174; DB 4; Length 335;
Best Local Similarity 23.5%; Pred. No. 1.2e-10;
Matches 81; Conservative 59; Mismatches 123; Indels
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STREET: Two Militia Drive
349 DYTSGAMLTGELKKALIEVLQPLIAEHQARRKEVTDEI 386
                                                   269 RYQRGGLGDVKTKRYLLEILERELGPIRERRIEFAKDM
                                                                                                                                                                                                                                                                                     Sequence 5784, Application US/09134000C Patent No. 6617156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Enterococcus faecalis
US-09-134-000C-5784
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US-08-743-130A-39
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TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
FILE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE OF INVENTION: PATHO0-07A

CURRENT APPLICATION NUMBER: US/09/583,110

PRIOR APPLICATION NUMBER: US 60/085,131

PRIOR FILING DATE: 1998-06-12

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

PRIOR PILING DATE: 1998-05-12

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PRIOR PILING DATE: 1998-05-13
                                                                                                                                                                                                                            PYFRMTRD------VAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIF 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIDIAKQIKTKVNKHAFSGGRDTIEEHRQFGGNCDVDVSFMYLTFF--LEDDDKLEQIRK 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 LADDADTLRKKVWSMYTDPDHIRVEDPGKIEGN----MVFHYLDVFGRPEDAQEIADMKE 268
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                                                                                                                                                                        143 GDAVEN------AKDIIACGFDINKTFIF--SDLDYMGMSSGFYKNVV---KIQK 186
                                                                                                                                                                                                                                                                                                                                             187 HVTFNQVKGIFGFTDSDCIGKISFPAIQAA--PSFSNSFPQIFRDRTDIQCLIPCAIDQD 244
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                                                        69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 RYQRGGLGDVKTKRYLLEILERELGPIRERRIEFAKDM 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 4392, Application US/09583110; Patent No. 6699703; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Streptococcus pneumoniae
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Best Local Similarity
Matches 81; Conserv
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US-09-583-110-4392
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JUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQNDAKRAGADVVKQVANPLLSGLI------YPLMQA-----IDEEHLG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 VDAQFG-GVDQRKIFVLABENLPSIGYKKRAHLMNPMVPGL-GQGGKM3ASDPNSKIDII 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 CDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGELKKALI----EVLQPLIAEHQARR 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 NVPLVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGF 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 YKNVVK----IQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTD 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 IQCLIPCAIDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DTAKQIKTKVNKHAFSGG--RDT--------IEEHRQFGGN 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---PLSY------DSIEQLKADFVDGKLAPPDLKSGVADKINELLAPIRAEFESS- 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CANDIDA TYROSYL-tRNA SYNTHETASE
PROTEINS, NUCLEIC ACIDS AND STRAINS COMPRISING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 IKDVLEKENRPVKIYWGTAPTGKP-HCGYFVPMIKLAHFLKAGCEVTVLLADLHAFLDNM 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.8%; Score 164.5; DB 2; Length 409; 20.7%; Pred. No. 1.9e-09; ve 59; Mismatches 132; Indels 107;
                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,130A FILING DATE: 01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 VLDAYENK-KPFYLYTGRGPSSEAMHVGHLIPFI---
                                                                                                                                                                                                        FILING DATE: 01-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brook EBG, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CP195-12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-6240
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TELEFAX: (617) 861-6240
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Patent No. 5871987
GENERAL INFORMATION:
APPLICANT: Gallant, Paul L.
APPLICANT: Shen, Xiaoyu
APPLICANT: Tao, Nianjun
APPLICANT: Tao, Nianjun
APPLICANT: Houman, Fariba
TITLE OF INVENTION: CANDIDA TYROSYI
TITLE OF INVENTION: PROTEINS, NUCLE
                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        380 KEVTDEIVKEFMTPRK 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           409 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 20.7%
Matches 78; Conservative
  Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
US-08-743-130A-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
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86 KAPLEVVKYRAKYYEFVVKAILKSINVPIERLKFVVGSSYQKGGDYV---MDLFKLSNIV 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 SONDAKRAGADVVKQVANPLLSGLI------YPLMQA------IDEEHLG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 IQCLIPCAIDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 VDAQFG-GVDQRKIFVLAEENLPSIGYKKRAHLMNPMVPGL-GQGGKMSASDPNSKIDII 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 VLDAYENK-KPFYLYTGRGPSSEAMHVGHLIPFI------FTKWLQDV-----F 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 NVPLVIQMTDDEKYLWKDLTLDQAYGDAVENAKDIIACGFDINKTFIFSDLDYMGMSSGF 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 409;
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.7%; Score 162.5; DB 2; Best Local Similarity 20.7%; Pred. No. 3.2e-09; Matches 78; Conservative 59; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                CORRENT AFFLICATION DATA:

CLASSIFICATION NUMBER: US/08/743,130A
FILING DATE: 01-NOV-1996
CLASSIFICATION: 435.
ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David E.
REGISTRATION UNMBER: 22,592
REGISTRATION UNMBER: CP195-12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ. ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: January 10, 2005, 21:24:32
Job time : 42 secs
                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       380 KEVTDEIVKEFMTPRK 395
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                                                                                        Lexington
Massachusetts
                                                                                                                                                USA
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                                                                                                                   STATE: Ma
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Sequence 10, Appl.
Sequence 11, Appl.
Sequence 10, Appl.
Sequence 10, Appl.
Sequence 1135, Appl.
Sequence 1235, Appl.
Sequence 128, Appl.
Sequence 128, Appl.
Sequence 12, Appl.
Sequence 16, Appl.
Sequence 16, Appl.
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Sequence 16, Appl.
Sequence 29813, Appl.
Sequence 29813, Sequence 29813, Sequence 14183, Sequence 145795, Appl.

4 US-10-080-839-1 5 US-10-240-532-10 6 US-09-919-039-163 4 US-10-247-671-166 6 US-10-247-671-166 6 US-10-733-963A-62 US-09-925-302-558 4 US-10-080-839-12 US-09-925-302-558 4 US-10-080-839-12 US-09-813-718-16 4 US-10-080-839-12 US-09-813-718-16 6 US-10-240-527A-16 6 US-10-240-527A-16 6 US-10-240-527A-16 7 US-10-240-527A-16 8 US-10-240-527A-16 9 US-10-240-527A-16 10S-10-240-527A-16 10S-10-25-30-146807 10S-10-25-30-855 10S-10-25-302-855 10S-10-25-302-855 10S-10-32-310-857 10S-10-425-115-29823 10S-10-425-115-29823 10S-10-425-115-29823 10S-10-425-115-29823 10S-10-425-115-29823 10S-10-425-115-29823 10S-10-425-115-29823

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2116
1 SNHGPDATEAEEDFVDPWTV......VTDEIVKGFMTPRKLSFDFQ 401
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1: \( \cgn2_6 \) ptodata/1 \) Pubpaa/USO7 \\ PUBCOMB.pep:*

2: \( \cgn2_6 \) ptodata/1 \) Pubpaa/PCT \\ Bay PUB. Pep:*

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                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                   - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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ALIGNMENTS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

 Result
 Query

 No.
 Score
 Match Length DB ID
 Description

 2
 2116 100.0
 401 4 US-10-080-839-13
 Sequence 13, Appl 2

 2
 2116 100.0
 415 9 US-09-813-718-14
 Sequence 14, Appl 3

 3
 2116 100.0
 415 14 US-10-080-839-5
 Sequence 14, Appl 4

 4
 2116 100.0
 415 15 US-10-240-523-14
 Sequence 14, Appl 5

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 2116 100.0
 437 15 US-10-240-527A-14
 Sequence 12, Appl 5

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 437 14 US-10-080-839-3
 Sequence 12, Appl 5

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 Sequence 12, Appl 5

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 Sequence 12, Appl 5

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 437 16 US-10-240-527A-12
 Sequence 12, Appl 11

 10
 2116 100.0
 471 14 US-10-126-467B-2
 Sequence 220, Appl 11

 11
 2116 100.0
 471 16 US-10-25-277-1234
 Sequence 250, App 11

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 471 17 US-10-370-715B-250
 Sequence 250, App 11

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APPLICANT: Schimmel, Paul
APPLICANT: Wakaugi, Keisuke
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
TITLE OF INVENTION: The Regulation of Angiogenesis
FILE REPERSIOE: TSI 720.1
CURRENT APPLICATION NATE: 2002-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 IDQDBYFRMTRDVAPRIGYPKPALLHSTFFFALQGAQTKMSASDPNSSIFLTDTAKQIKT 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 FIRRGIFFSHRDMNQVLDAXENKKPFYLXTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Cleavage Product T1 of recombinant human TrpRS
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Best Local Similarity 100.0%; Score 2116; DB 14; Length 415;
Best Local Similarity 100.0%; Pred. No. 4.1e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 KKALIEVLOPLIAEHOARRKEVTDEIVKEFMTPRKLSFDFQ 401
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Publication No. US20040009163A1
GENERAL INFORMATION:
APPLICANT: Schimmel, Paul
APPLICANT: Wakasugi, Kaisuke
TITLE OF INVENTION: Human Aminoacyl-tR
TITLE OF INVENTION: The Regulation of
TITLE REFERENCE: TSRI 720.1
FILE REFERENCE: TSRI 720.1
CURRENT APPLICATION NUMBER: US/10/240,
CURRENT FILING DATE: 2002-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
US-10-240-532-14
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| Sequence 14, Application US/09913718
| Publication No. US20020182666A1
| GENERAL INFORMATION:
| APPLICANT: Schimmel, Paul
| APPLICANT: Wakasugi, Keisuke
| TITLE OF INVENTION: The Regulation of Anglogenesis
| TITLE OF INVENTION: The Regulation of Anglogenesis
| TITLE OF INVENTION: The Regulation of Anglogenesis
| CURRENT APPLICATION NUMBER: US/09/813,718
| CURRENT APPLICATION NUMBER: US/09/813,718
| CURRENT PILING DATE: 2001-03-21
| NUMBER OF SEQ ID NOS: 58
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 44
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100.0%; Pred. No. 4.1e-194;
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 401; Conservative
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Sequence 14, Application US/10240527A

Publication No. US20040152079A1

GENERAL INFORMATION:

APPLICANT: SCHIMMEL, Paul

APPLICANT: WAKASUGI, Keisuke

TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase

TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase

TITLE OF INVENTION: Polypeptides Useful for the Regulation of Angiogenesis

FILE REFERENCE: TSRI 720.2

CURRENT APPLICATION NUMBER: US/10/240,527A

PRIOR FILING DATE: 2000-09-30

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2000-03-31

NUMBER OF SEQ ID NOS: 58

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14

LENGTH: 415
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                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: human OTHER INFORMATION: supermini TrpRS in pET20B
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                                                                                                                                                                                                                                                                      100.0%; Score 2116; DB 15; 100.0%; Pred. No. 4.1e-194;
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US-10-240-527A-14
                                                                                                                                                                                                                                                                                                         0; Mismatches
PRIOR APPLICATION NUMBER: PCT/US01/08975
PRIOR APPLICATION NUMBER: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/193,471
PRIOR APPLICATION NUMBER: 2000-03-31
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
                                                                                                                                                               ORGANISM: Artificial Sequence
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ORGANISM: Artificial Seguence
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Best Local Similarity 100.
Matches 401; Conservative
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US-10-240-527A-14
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APPLICANT: Schimmel, Paul
APPLICANT: Schimmel, Paul
APPLICANT: Wakaeugi, Keisuke
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
TITLE OF INVENTION: The Regulation of Angiogenesis
FILE REPERBNCE: 00-221
CURRENT APPLICATION NUMBER: US/09/813,718
CURRENT FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
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US-09-813-718-12
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Query Match 100.0%; Score 2116; DB 16; Best Local Similarity 100.0%; Pred. No. 4.1e-194; Matches 401; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-813-718-12; Sequence 12, Application US/09813718; Publication No. US20020182666A1; GENERAL INFORMATION:
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Matches 401, Conservative
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VVKIOKHVTFNOVKGIFGFTDSDCIGKISFPAIOAAPSFSNSFPOIFRDRTDIOCLIPCA

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Sequence 12, Application US/10240532
Publication No. US20040009163A1
GENERAL INFORMATION:
APPLICANT: Schimmel, Paul
APPLICANT: Waksugi, Keisuke
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
TITLE OF INVENTION: Humans: Use 10.10/240,532
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: DCT/US01/08975
PRIOR APPLICATION NUMBER: 2001-03-21
PRIOR APPLICATION NUMBER: 2001-03-21
PRIOR APPLICATION NUMBER: 2000-03-31
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 437
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Publication No. US20040152079A1
GENERAL INFORMATION:
APPLICANT: SCHIMMEL, Paul
TITLE OF INVENTION: Howan Aminoacyl-tRNA Synthetase
TITLE OF INVENTION: Polypeptides Useful for the Regulation of Angiogenesis
FILE REPERENCE: TSRI 720.2
CURRENT APPLICATION NUMBER: US/10/240,527A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: human mini
OTHER INFORMATION: TrpRS in pET20B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 2116; DB 15; Length 437; 100.0%; Pred. No. 4.4e-194; ive 0; Mismatches 0; Indels 0;
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Matches 401; Conservative
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APPLICANT: Friedlander, Martin
TITLE OF INVENTION: Tryptophanyl-tRNA Synthetase Derived
TITLE OF INVENTION: Tryptophanyl-tRNA Synthetase Derived
TITLE OF INVENTION: Tryptophanyl-tRNA Synthetase Derived
TITLE OF INVENTION: Tryptophanyl-tRNA Synthetase Derived
CURRENT APPLICATION UNMBER: US/10/080,839
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 60/270,951
PRIOR APPLICATION NUMBER: 60/270,951
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FRASESQ for Windows Version 4.0
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VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA 263
                                                                                                       IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 323
                                                                                                                                                                                                              KVNKHAPSGGRDTIEEHRQFGGGCDVDVSFMYLTFFLEDDDKLEQIRKDYTSGAMLTGEL 383
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                                                                            241 IDQDPYFRMTRDVAPRIGYPKPALLHSTFFPALQGAQTKMSASDPNSSIFLTDTAKQIKT 300
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Best Local Similarity 100.0%; Pred. No. 4.4e-194;
Matches 401; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: human mini TrpRS in pET20B
US-10-080-839-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 3, Application US/10080839; Publication No. US20030017564A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Schimmel, Paul
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US-10-080-839-3
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LENGTH: 437
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APPLICANT: Matray, Richard,
APPLICANT: Wateon, Susan R.
APPLICANT: Wateon, Susan R.
APPLICANT: Wateon, Susan R.
TITLE OF INVENTION: Methods of Diagnosis of Cancer,
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-11-12
PRIOR FILING DATE: 2001-11-12
PRIOR PLOATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-29
PRIOR FILING DATE: 2001-11-24
PRIOR FILING DATE: 2001-11-24
PRIOR FILING DATE: 2002-01-08
PRIOR PLING DATE: 2002-01-08
PRIOR FILING DATE: 2002-01-08
PRIOR FILING DATE: 2002-01-08
PRIOR FILING DATE: 2002-02-03
PRIOR PLING DATE: 2002-02-03
PRIOR APPLICATION NUMBER: US 60/347,319
PRIOR FILING DATE: 2002-01-08
PRIOR PLING DATE: 2002-02-03
PRIOR APPLICATION NUMBER: US 60/355,714
PRIOR PLING DATE: 2002-02-03
                                                                                                                                                                                                           131 FLRRGIFFSHRDMNQVLDAYENKKPFYLYTGRGPSSEAMHVGHLIPFIFTKWLQDVFNVP
                                                                                                                                                                                                                                                                                                                                                                                                                               251 VVKIQKHVTFNQVKGIFGFTDSDCIGKISFPAIQAAPSFSNSFPQIFRDRTDIQCLIPCA
                                                                           1 SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH
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                               Gaps
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Remaining Prior Application data removed - See File Wrapper or PALM.
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       Pred. No. 4.9e-194;
                            0; Mismatches
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  100.0%;
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APPLICANT: Aziz, Netesha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
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Hevezi, Peter A.
Mack, David H.
                            Matches 401; Conservative
     Best Local Similarity
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APPLICANT:
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| Sequence 2. Application No. US20030059797A1
| GENERAL INFORMATION:
| APPLICANT: Paley, Elena
| TILL OF INVENTION: ALONE NUMBER: US/10/126,467B
| TILL OF INVENTION NUMBER: US/10/126,467B
| CURRENT FILING DATE: 2002-11-19
| CURRENT FILING DATE: 2001-04-19
| PRIOR APPLICATION NUMBER: 60/284,980
| PRIOR PELING DATE: 2001-02-28
| PRIOR APPLICATION NUMBER: 09/513,895
| PRIOR FILING DATE: 2000-02-28
| PRIOR FILING DATE: 1999-08-27
| NUMBER OF SEQ ID NOS: 6
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 2
| LENGTH: A71
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100.0%; Pred. No. 4.4e-194;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                    , OTHER INFORMATION: Human mini TrpRS in pET20B
US-10-240-527A-12
                    PRIOR APPLICATION NUMBER: PCT/USO1/08966
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US 60/193,471
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
     2002-09-30
                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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ORGANISM: Homo sapiens
CURRENT FILING DATE:
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Best Local Similarity
Matches 401; Conserv
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Patin Docket Preview

APPLICANT: BODARY, SARAH C.

APPLICANT: BRISDELL, HUNET

APPLICANT: BRISDELL, HUNET

APPLICANT: JACKMAN, JANET

APPLICANT: JACKMAN, JANET

APPLICANT: WILLIAMS, P. MICKEY

APPLICANT: WU, THOMAS, P. MICKEY

APPLICANT: WU, THOMAS, D.

TITLE OF INVENTION: Related Diseases

FILE REFERENCE: P1948R1-US

CURRENT FILING DATE: 2003-02-21

NUMBER OF SEQ ID NOS: 742

SEQ ID NO 250
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; Publication No. US20040258678A1
; GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 401; Conservative
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US-10-370-715B-250
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TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
TITLE OF INVENTION: PATHWAY
FILE OF INVENTION: PATHWAY
FILE REPERENCE: D0284 NP
CURRENT APPLICATION NUMBER: US/10/755,889
CURRENT FILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: U.S. 60/440,068
PRIOR APPLICATION NUMBER: U.S. 60/469,757
PRIOR APPLICATION NUMBER: U.S. 60/469,757
NUMBER OF SEQ ID NOS: 823
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 250
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                                                                                                                                                     Length 471;
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                                                                                                                                                   100.0%; Score 2116; DB 14; 100.0%; Pred. No. 4.9e-194;
                                                                                                                                                                                        0; Mismatches
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                     SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1234
                                                                                                                                                                                        Matches 401; Conservative
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     NUMBER OF SEQ ID NOS: 1386
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; ORGANISM: Homo sapiens
US-10-755-889-250
                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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Matches 401; Conserv
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US-10-755-889-250
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             APPLICANT: Wakasugi, Ketsuke
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For
TITLE OF INVENTION: The Regulation of Angiogenesis
FILE REPERENCE: 00-221
CURRENT APPLICATION NUMBER: US/09/813,718
CURRENT FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SNHGPDATEAEEDFVDPWTVQTSSAKGIDYDKLIVRFGSSKIDKELINRIERATGQRPHH 130
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100.0%; Score 2116; DB 9; Length 484;
Best Local Similarity 100.0%; Pred. No. 5.1e-194;
Matches 401; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: human
OTHER INFORMATION: full-length TrpRS in pET208
US-09-813-718-10
                                                                                   431 KKALIEVLQPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 471
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                                                                 KKALIEVLOPLIAEHQARRKEVTDEIVKEFMTPRKLSFDFQ 401
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Sequence 10, Application US/09813718
Publication No. US20020182666A1
FEBERAL INFORMATION:
APPLICANT: Schimmel, Paul
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TYPE: PRT
ORGANISM: Artificial Sequence
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RNA Synthetase Derived
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APPLICANT: Friedlander, Martin
TITLE OF INVENTION: Tryptophanyl-tRNA Synther
TITLE OF INVENTION: Polypeptides Useful For
FILE REFERENCE: TSRI-813.1
CURRENT APPLICATION NUMBER: US/10/080,839
CURRENT FILING DATE: 2002-02-22
FRIOR APPLICATION NUMBER: 60/270,951
PRIOR FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Recombinant human trpRS US-10-080-839-1
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ORGANISM: Artificial Sequence
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